

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:35:27 ; Search time 170 Seconds
(without alignments)
1114.525 Million cell updates/sec

Title: US-10-606-055-2
Perfect score: 370
Sequence: 1 MRLIFVYTLICANFCSRD.....DIQLDHERCDCICSSRPPR 370

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 5

Total number of hits satisfying chosen parameters: 93916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	100.0	370	2	Q9GZP0
2	323	87.3	364	2	Q9BWS5
3	35	9.5	300	2	Q6V9H4
4	32	8.6	370	2	Q9EQT1
5	27	7.3	261	2	Q8K2L3
6	27	7.3	370	2	Q9Z5I7
7	9	2.4	77	2	Q93XZ2
8	9	2.4	77	2	Q75NH6
9	9	2.4	79	2	Q9ZRV0
10	8	2.2	76	2	O22492
11	8	2.2	76	2	O22581
12	8	2.2	76	2	Q9M4N0
13	8	2.2	77	1	MT2_VICFA
14	8	2.2	77	1	MTA_TRIRP
15	8	2.2	77	2	Q8S3M2
16	8	2.2	77	2	Q61674
17	8	2.2	77	2	Q9AR26
18	8	2.2	77	2	Q9SNG3
19	8	2.2	77	2	Q9ZNT5
20	8	2.2	78	1	MT2_NICGU
21	8	2.2	78	2	Q93WV3
22	8	2.2	78	2	Q94G67
23	8	2.2	78	2	Q6L8H8
24	8	2.2	78	2	Q6PML3
25	8	2.2	78	2	Q8GTD0
26	8	2.2	79	1	MT2_CICAR
27	8	2.2	79	2	Q80335
28	8	2.2	79	2	Q944W1
29	8	2.2	79	2	Q6PML4
30	8	2.2	79	2	Q75NH4
31	8	2.2	79	2	Q75NH9

ALIGNMENTS

32	8	2.2	79	2	Q75NI1	Q75ni1 glycine max
33	8	2.2	79	2	Q75NI3	Q75ni3 phaseolus a
34	8	2.2	79	2	Q7M213	Q7m213 glycine max
35	8	2.2	79	2	Q9AU16	Q9au16 typha latif
36	8	2.2	79	2	Q9AXE5	Q9axe5 avicennia m
37	8	2.2	79	2	Q9FQ79	Q9fq79 musa acumin
38	8	2.2	80	1	MT1_COPAR	P43396 coffea arab
39	8	2.2	80	1	MT21_BRAJU	P56168 brassica ju
40	8	2.2	80	1	MT23_BRAJU	P56170 brassica ju
41	8	2.2	80	1	MT25_BRAJU	P56172 brassica ju
42	8	2.2	80	1	MT2_BRARA	Q42494 brassica ra
43	8	2.2	80	1	MT2_BRARP	Q39289 brassica ra
44	8	2.2	80	1	MT3_RICCO	P30564 ricinus com
45	8	2.2	80	2	O04107	O04107 oryza sativ
46	8	2.2	80	2	O04688	O04688 mesembryant
47	8	2.2	80	2	O22488	O22488 oryza sativ
48	8	2.2	80	2	Q7XAF3	Q7xaf3 pringlea an
49	8	2.2	80	2	Q8GTC9	Q8gtc9 hordeum vul
50	8	2.2	80	2	Q9FR40	Q9frm97 brassica ol
51	8	2.2	80	2	Q9M697	P25860 arabidopsis
52	8	2.2	81	1	MT2A_ARATH	P63958 xerophyta h
53	8	2.2	81	2	Q6J9F8	O6p24 cynodon dac
54	8	2.2	81	2	Q6PW24	P94029 oryza sativ
55	8	2.2	82	1	MT21_ORYSA	Q40158 lycopersico
56	8	2.2	82	1	MT2B_LYCES	Q7f7x9 oryza sativ
57	8	2.2	82	2	Q9SPE7	Q9spe7 ipomoea bat
58	8	2.2	82	2	Q9SPE7	P93433 oryza sativ
59	8	2.2	84	1	MT22_ORYSA	O65xv5 oryza sativ
60	8	2.2	84	2	Q65XV5	Q7x9m0 triticum ae
61	8	2.2	114	2	Q7X9M0	Q8xiq7 clostridium
62	8	2.2	124	2	Q8XIQ7	Q94ct9 oryza sativ
63	8	2.2	136	2	Q94CT9	Q9f8c4 streptococc
64	8	2.2	174	2	Q9F8C4	Q8elc6 streptococc
65	8	2.2	174	2	Q8E1C6	Q8e6u3 streptococc
66	8	2.2	174	2	Q8E6U3	Q84684 peanut chlo
67	8	2.2	220	2	Q84684	Q9nra1 homo sapien
68	8	2.2	345	2	Q9NRA1	Q9ui22 homo sapien
69	8	2.2	345	2	Q9EQX6	Q9eqx6 rattus norv
70	8	2.2	345	2	Q9UL22	Q9jvh8 mus musculu
71	8	2.2	345	2	Q9JHV8	Q9qv71 m fallotein
72	8	2.2	345	2	Q9QV71	Q8c119 mus musculu
73	8	2.2	345	2	Q8C119	Q9i946 gallus gall
74	8	2.2	345	2	Q9I946	Q8y7c9 listeria mo
75	8	2.2	353	2	Q8Y7C9	Q92c00 listeria in
76	8	2.2	353	2	Q92C00	Q71zw8 listeria mo
77	8	2.2	353	2	Q71ZW8	P21307 zymomonas m
78	8	2.2	485	1	G6PD_ZYMMO	Q49067 zea mays (m
79	8	2.2	531	2	O49067	Q76267 bacterioph
80	8	2.2	772	2	Q76267	Q8i734 trypanosoma
81	8	2.2	850	2	Q7KU82	P91638 drosophila
82	8	2.2	935	2	Q8I734	Q9v862 drosophila
83	8	2.2	944	2	Q9V862	Q8y469 listeria mo
84	8	2.2	944	2	Q9V862	Q927q7 listeria in
85	8	2.2	995	2	Q8Y469	Q71wj3 listeria mo
86	8	2.2	995	2	Q927Q7	Q7q5u3 anopheles g
87	8	2.2	995	2	Q71WJ3	P35590 homo sapien
88	8	2.2	1072	2	Q7Q5U3	Q86a63 dictyosteli
89	8	2.2	1138	2	TIE1_HUMAN	Q8gsp2 streptomyce
90	8	2.2	1318	2	O86A53	Q65va7 manheimia
91	8	2.2	7349	2	Q8GSP2	Q9us95 schizosacch
92	8	2.2	35	2	Q65VA7	O22319 musa acumin
93	7	1.9	66	2	Q9USS5	Q22319 musa acumin
94	7	1.9	78	1	MT2_MUSAC	Q94198 atropa bell
95	7	1.9	82	2	Q94T98	Q95r16 caenorhabdi
96	7	1.9	86	2	Q95R16	Q8h9n2 lactococcus
97	7	1.9	98	2	Q8H9H2	Q7xhj3 quercus rob
98	7	1.9	99	2	Q7XJ3	Q7pe07 anopheles g
99	7	1.9	99	2	Q7BE07	Q94m87 lactococcus
100	7	1.9	99	2	Q94M87	

```
RESULT 1
Q9GZP0
ID Q9GZP0 PRELIMINARY; PRT; 370 AA.
AC Q9GZP0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Spinal cord-derived growth factor-B (MSTP036) (Platelet-derived growth
factor D) (Iris-expressed growth factor long form).
GN Name=hSCDGF-B; Synonyms=IEGF, PDGFD;
OS Homo sapiens (Human)
OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
SCDGF/PDGF-C/fallotain.";
RT Biochem. Biophys. Res. Commun. 280:733-737(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
EX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
RA LaRoche W.J., Jeffers M., McDonald W.F., Challa K.R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez E., Degler L.L., Rittman B., Shimkets J.,
RA Shimkets R.A., Rothberg J.M., Lichtenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor.";
RL Nat. Cell Biol. 3:517-521(2001).
RN [4]
RP SEQUENCE FROM N.A.
EX PubMed=11331881; DOI=10.1038/35074588;
RA Bergsten E., Uetela M., Li X., Pietras K., Ostman A., Heidin C.H.,
RA Allitalo K., Eriksson U.;
RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
receptor.";
RL Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RA Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
RA Bouffard G., Smith D., Peterson K.;
RT "Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium.";
RL Mol. Vision 8:185-195(2002).
DR EMBL; AB033832; BAB18903.1; -
DR EMBL; AF113216; AAG39287.1; -
DR EMBL; AF335584; AAK38840.1; -
DR EMBL; AF336376; AAK56136.1; -
DR EMBL; AY027517; AAK20081.1; -
DR PIR; JC7591; JC7591.
DR HSSP; Q9JUS8; 1N70.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD growth factor.
DR Efam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF 2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674_CRC64;
Query Match 100.0%; Score 370; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRILFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESHTLDLYRDETIOVKG 60
DB 1 MHRILFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESHTLDLYRDETIOVKG 60
QY 61 NGYVQSPFPNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLSEANDICRYDFVEVEDIS 120
DB 61 NGYVQSPFPNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLSEANDICRYDFVEVEDIS 120
QY 121 ETSTIIRGRWCGHKHEVPPRIKSRNTQIKITFKSDDYFVAKFGFKIYYSLLEDFOQAAASE 180
DB 121 ETSTIIRGRWCGHKHEVPPRIKSRNTQIKITFKSDDYFVAKFGFKIYYSLLEDFOQAAASE 180
QY 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSHQEDLENNY 240
DB 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSHQEDLENNY 240
QY 241 LDTPRYGRSYHDKRSKVDLDRLNDDAKRYSCYCTPRNYSVINREELKLANVVFPPRCLLVQ 300
DB 241 LDTPRYGRSYHDKRSKVDLDRLNDDAKRYSCYCTPRNYSVINREELKLANVVFPPRCLLVQ 300
QY 301 RCGNGCGGTVNRSCYCTNSGKTVKKYHEVLFQFPGHIKRRGRKTMALVDIQLDHHERC 360
DB 301 RCGNGCGGTVNRSCYCTNSGKTVKKYHEVLFQFPGHIKRRGRKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPPR 370
DB 361 DCICSSRRPPR 370
RESULT 2
Q9BWV5
ID Q9BWV5 PRELIMINARY; PRT; 364 AA.
AC Q9BWV5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Iris-expressed growth factor short form (Platelet derived growth
factor D, isoform 2) (SCDGF-B).
GN Name=IEGF; Synonyms=PDGFD; ORFNames=UNQ1899;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RX MEDLINE=2103462; PubMed=12107412;
RA Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
RA Bouffard G., Smith D., Peterson K.;
RT "Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium.";
RL Mol. Vision 8:185-195(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
```

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maria M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=Testis;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh V., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY027518; AAK20082.1; -;
DR EMBL; BC030645; AAH3645.1; -;
DR EMBL; AY359116; AAQ89474.1; -;
DR PIR; JC7591; JC7591.
DR HSSP; Q9JJJ8; 1NT0.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0008083; F.growth factor activity; IEA.
DR GO; GO:0008151; P.cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR FT NON_TER 1 300
DR FT NON_TER 300 300
SQ SEQUENCE 364 AA; 42166 MW; 245C53E8DDEA9EAC CRC64;
Query Match 87.3%; Score 323; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 DLYRDETQVKGNGVQSPFPNSYPRNLLTTLRLHSGQENTRIQLVFNQFGLGEAEND 107
DB 42 DLYRDETQVKGNGVQSPFPNSYPRNLLTTLRLHSGQENTRIQLVFNQFGLGEAEND 101
QY 108 ICRYDFVEVEDISESTIIRGWCWGHEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYY 167
DB 102 ICRYDFVEVEDISESTIIRGWCWGHEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYY 161
QY 168 SLEDFQPAASFTNWSVTSSISGVSYNSPSTVDTPLTADALDKIAEFDVTELLKYF 227
DB 162 SLEDFQPAASFTNWSVTSSISGVSYNSPSTVDTPLTADALDKIAEFDVTELLKYF 221
QY 228 NPESWQEDLENMYLDTPRYGRSGSYHDKSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKL 287
DB 222 NPESWQEDLENMYLDTPRYGRSGSYHDKSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKL 281
QY 288 ANWFFPRCLLVQRCGCGCGCTVNRSCITSCNGTKVKKYHEVLQFEPGHIKRRGRAKTM 347
|||||

DB 282 ANWFFPRCLLVQRCGCGCGCTVNRSCITSCNGTKVKKYHEVLQFEPGHIKRRGRAKTM 341
QY 348 ALVDIQLDHHERCDCICSRPPR 370
|||||
DB 342 ALVDIQLDHHERCDCICSRPPR 364
|||||
RESULT 3
Q9EQTH PRELIMINARY; PRT; 300 AA.
ID Q6V9H4
AC Q6V9H4; (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Iris-expressed growth factor (Fragment).
GN Name=PDGFD;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Ray S., Wistow G.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY347260; AAQ24382.1; -;
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0008083; F.growth factor activity; IEA.
DR GO; GO:0008151; P.cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR FT NON_TER 1 300
DR FT NON_TER 300 300
SQ SEQUENCE 300 AA; 34616 MW; 716C873C9C01C0C6 CRC64;
Query Match 9.5%; Score 35; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 YGRSYHDKRSKVDLDRNLDDAKRYSCPTPRNYSVN 280
DB 190 YGRSYHDKRSKVDLDRNLDDAKRYSCPTPRNYSVN 224
|||||
RESULT 4
Q9EQTH PRELIMINARY; PRT; 370 AA.
ID Q9EQTH
AC Q9EQTH; (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal-cord derived growth factor-B.
GN Name=rSCDGF-B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hamada T., Ui-Tei K., Inaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
RL SCDGF/PDGF-C/fallicotin";
DR Biochem. Biophys. Res. Commun. 280:733-737(2001).
DR PIR; JC7592; JC7592.
DR HSSP; Q9UCV4; 1NZI.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0008083; F.growth factor activity; IEA.
DR GO; GO:0008151; P.cell growth and/or maintenance; IEA.
DR

DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000072; PD_growth_factor.
 DR Pfam; PF00431; CUB; 1.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00141; PDGF; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS0278; PDGF 2; 1.
 SQ SEQUENCE 370 AA; 42809 MW; 7BB8A251F679BF73 CRC64;

Query Match 8.6%; Score 32; DB 2; Length 370;
 Best Local Similarity 100.0%; Pred. No. 4.4e-24;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 ATPQSASIKALRNANLRDESNHLDLYRRDE 54
 |||||
 DB 23 ATPQSASIKALRNANLRDESNHLDLYRRDE 54

RESULT 5

O8K2L3 ID O8K2L3 PRELIMINARY; PRT; 261 AA.
 AC O8K2L3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Pdgd protein.
 GN Name=pgd;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;
 RX STRAUSBERG R.;
 RL SUBMITTED (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC030896; AAH30896.1; -.
 DR HSSP; Q9JUS8; INT0.
 DR MGD; MG1:1919035; Pdgd.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IDA.
 DR InterPro; IPR000859; CUB.
 DR Pfam; PF00431; CUB; 1.
 DR SMART; SM00042; CUB; 1.
 DR PROSITE; PS01180; CUB; 1.
 SQ SEQUENCE 261 AA; 30228 MW; 2BEC3F6373A52D09 CRC64;

Query Match 7.3%; Score 27; DB 2; Length 261;
 Best Local Similarity 100.0%; Pred. No. 5.1e-19;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 142 SRTNQIKITKSDDDYFVAKGCFKIYYS 168
 |||||
 DB 142 SRTNQIKITKSDDDYFVAKGCFKIYYS 168
 |||||
 RESULT 6
 Q92517 ID Q92517 PRELIMINARY; PRT; 370 AA.
 AC Q92517; Q9DIL8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Platelet-derived growth factor D (Mus musculus 18-day embryo whole
 body cDNA, RIKEN full-length enriched library, clone:1110003I09
 product:platelet-derived growth factor D).
 DE Name=Pgfd;
 GN Name=Pgfd;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
 RA LaRoche W.J., Jeffers M., McDonald W.F., Chiklaku R.A.,
 RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
 RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
 RA Shimkets R.A., Rothberg J.M., Lichtenstein H.S.;
 RT "PDGF D, A Novel Protease-Activated Growth Factor.";
 RL Nat. Cell Biol. 3:517-521 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:695-690 (2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX STRAIN=C57BL/6J; TISSUE=Whole body;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,


```

RESULT 8
Q75NH6 PRELIMINARY; PRT; 77 AA.
ID Q75NH6 AC Q75NH6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Type 2 metallothionein.
GN Name=MET;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RA Sun X., Xian X., Hong K., Kajiwuchi T.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB176565; BAD18383.1; -
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1_15p.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 77 AA; 7728 MW; 7D7911A020BD903C CRC64;

Query Match 2.4%; Score 9; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGGGT 310
DB 4 CGGNCGGGT 12

RESULT 9
Q9ZRV0 PRELIMINARY; PRT; 79 AA.
ID Q9ZRV0 AC Q9ZRV0;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Metallothionein-like protein class II.
OS Fagus sylvatica (beechnut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fagales; Fagaceae; Fagus.
NCBI_TaxID=28930;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Seeds;
RC MEDLINE=99372458; PubMed=10447467;
RX Calvo A.P., Lorenzo O., Nicolas C., Nicolas G., Rodriguez D.;
RT "Characterization of a Metallothionein-coding cDNA (Accession No.
RL Plant Physiol. 120:633-633(1999).
DE EMBL; AJ130886; CAA10232.1; -
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 79 AA; 7773 MW; 5936D779AF56D6C4A CRC64;

Query Match 2.4%; Score 9; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGGGT 310
DB 4 CGGNCGGGT 12

```

```

RESULT 10
O22492 PRELIMINARY; PRT; 76 AA.
ID O22492;
AC O22492;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Metallothionein-1 like protein.
OS Oenanthse javanica (water celery) (Water dropwort).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Apiales; Apiaceae; Apioideae; Oenantheae; Oenanthae.
OX NCBI_TaxID=49556;
RN [1]
RP SEQUENCE FROM N.A.
RA Min B., Lee S.Y.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF017787; AAB70560.1;
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metalthion_15p.
DR Pfam; PF01439; Metalthio_2; 1.
DR ProDom; PD001611; Metalthion_15p; 1.
SQ SEQUENCE 76 AA; 7319 MW; DDF0A352D9448404 CRC64;

Query Match 2.2%; Score 8; DB 2; Length 76;
Best Local Similarity 100.0%; Pred.No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 11
O82581 PRELIMINARY; PRT; 76 AA.
ID O82581;
AC O82581;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Metallothionein-1-like protein.
OS Pimpinella brachycarpa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Apiales; Apiaceae; Apioideae; apioid superciade;
OC Pimpinella clade; Pimpinella.
OX NCBI_TaxID=45043;
RN [1]
RP SEQUENCE FROM N.A.
RA Cho J.-I., Lee K.-W.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF093585; AAC62510.1;
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metalthion_15p.
DR Pfam; PF01439; Metalthio_2; 1.
DR ProDom; PD001611; Metalthion_15p; 1.
SQ SEQUENCE 76 AA; 7419 MW; B80BFD32D95892D8 CRC64;

Query Match 2.2%; Score 8; DB 2; Length 76;
Best Local Similarity 100.0%; Pred.No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 12
Q9M4N0 PRELIMINARY; PRT; 76 AA.
ID Q9M4N0;
AC Q9M4N0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

```

```

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Metallothionein-like protein type 2 (Fragment).
GN Name=mt2;
OS Persea americana (Avocado).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae; Persea.
OX NCBI_TaxID=3435;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fruit mesocarp;
RA Zamorano J.P., Evans A.D., Dopico B., Lowe A.L., Wilson I.D.,
RA Merodio C., Grieron D.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133145; CAB77242.1;
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metalthion_15p.
DR Pfam; PF01439; Metalthio_2; 1.
DR ProDom; PD001611; Metalthion_15p; 1.
FT NON TER 1
SQ SEQUENCE 76 AA; 7568 MW; A6433B2965E1566D CRC64;

Query Match 2.2%; Score 8; DB 2; Length 76;
Best Local Similarity 100.0%; Pred.No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 1 CGGNCGCG 8

RESULT 13
MT2_VICFA STANDARD; PRT; 77 AA.
ID MT2_VICFA
AC Q41657;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Metallothionein-like protein type 2.
GN Name=MTI;
OS Vicia faba (Broad bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Vicia.
OX NCBI_TaxID=3306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95036014; PubMed=7948889;
RA Foley R.C., Singh K.B.;
RT "Isolation of a Vicia faba metallothionein-like gene: expression in
RT foliar trichomes."
RL Plant Mol. Biol. 26:435-444(1994).
CC -!- FUNCTION: Metallothioneins have a high content of cysteine
CC residues that bind various heavy metals.
CC -!- TISSUE SPECIFICITY: Expressed in the left, stem and flower, at
CC very low levels in roots and is not detectable in mesophyll
CC protoplasts.
CC -!- SIMILARITY: Belongs to the metallothionein superfamily. Family 15.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; X77254; CAA54471.1;
DR PIR; S52636; S52636.
DR InterPro; IPR000347; Metalthion_15p.
DR Pfam; PF01439; Metalthio_2; 1.
DR ProDom; PD001611; Metalthion_15p; 1.
KW Metal-binding; Metal-thiolate cluster; Multigene family.
SQ SEQUENCE 77 AA; 7730 MW; 7D7BAD8D0223BF3C CRC64;

```

```
Query Match          2.2%; Score 8; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGCG 309
   |||||
Db 4 CGGNCGCG 11

RESULT 14
MTA_TRIP
ID MTA_TRIP STANDARD; PRT; 77 AA.
AC P43398;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Metallothionein-like protein A (MT-A).
GN Name=MTA;
OS Trifolium repens (Creeping white clover).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Trifolium.
OX NCBI_TaxID=3899;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Huia; TISSUE=stolon node;
RA Ellison N.W., White D.W.R.;
RT "Isolation of two cDNA clones encoding metallothionein-like proteins
from Trifolium repens L.";
RL (er) Plant Gene Register PGR96-068.
CC -!- FUNCTION: Metallothioneins have a high content of cysteine
residues that bind various heavy metals.
CC -!- SIMILARITY: Belongs to the metallothionein superfamily. Family 15.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z26492; CAA81264.1; -
DR PIR; S37239; S37239.
DR InterPro; IPR000347; Metallthion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
KW Metal-binding; Metal-thiolate cluster; Multigene family.
SQ SEQUENCE 77 AA; 7503 MW; 5F4C163BA644B8D1 CRC64;

Query Match          2.2%; Score 8; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGCG 309
   |||||
Db 4 CGGNCGCG 11

RESULT 15
Q8S3M2
ID Q8S3M2 PRELIMINARY; PRT; 77 AA.
AC Q8S3M2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Metallothionein-like protein 2.
GN Name=A2MT2;
OS Azolla filiculoides (Water fern).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Monilliformopses; Filicophyta; Filicopsida; Hydropteridales;
OC Azollaceae; Azolla.
```

```
OX NCBI_TaxID=84609;
RN [1]
RP SEQUENCE FROM N.A.
RA Schor T., Goldsbrough P.B., Adam Z., Tel-Or E.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF482470; AAL85416.1; -
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallthion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
SQ SEQUENCE 77 AA; 7839 MW; 54DDF0CC032F50D5 CRC64;

Query Match          2.2%; Score 8; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGCG 309
   |||||
Db 4 CGGNCGCG 11

RESULT 16
Q6I674
ID Q6I674 PRELIMINARY; PRT; 77 AA.
AC Q6I674;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Type-2 metallothionein.
GN Name=CLMT2;
OS Citrullus lanatus (Watermelon) (Citrullus vulgaris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Citrullus.
OX NCBI_TaxID=3654;
RN [1]
RP SEQUENCE FROM N.A.
RA Akashi K.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB182918; BAD26571.1; -
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallthion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 77 AA; 7805 MW; 6E75AB740535B64 CRC64;

Query Match          2.2%; Score 8; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGCG 309
   |||||
Db 4 CGGNCGCG 11

RESULT 17
Q9AR26
ID Q9AR26 PRELIMINARY; PRT; 77 AA.
AC Q9AR26;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Class I type 2 metallothionein.
OS Avicennia marina (Grey mangrove).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Lamiales; Acanthaceae; Acanthaceae incertae sedis; Avicennia.
OX NCBI_TaxID=82927;
RN [1]
RP SEQUENCE FROM N.A.
RA Parani M., Parida A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
```

```

RA Parani M., Parida A.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF334141; AAK11269.1; -.
DR EMBL; AF329968; AAG61122.1; -.
GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 77 AA; 7650 MW; 421A2B2DAF1382AF CRC64;

Query Match 2.2%; Score 8; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 18
Q9SMG3 PRELIMINARY; PRT; 77 AA.
AC Q9SMG3;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Metallothionein.
GN Name=MT1;
OS Eichhornia crassipes (Water hyacinth).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Commelinales;
OC Pontederiaceae; Eichhornia.
OX NCBI_TaxID=44947;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
RA Kong K.F., Teang J.S.H.;
RT "Nucleotide Sequences of Genomic Clones (Accession Nos. AJ247090,
RT AJ247195 and AJ247196) Encoding a Type 2 Metallothionein-like Protein
RT from Water Hyacinth (Eichhornia crassipes). (FGR99-143).";
RL Plant Physiol. 121:313-313(1999).
DR EMBL; AJ010162; CAA09025.1; -.
DR EMBL; AJ010160; CAA09023.1; -.
DR EMBL; AJ010161; CAA09024.1; -.
DR EMBL; AJ247090; CAB53390.1; -.
DR EMBL; AJ247196; CAB53392.1; -.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 77 AA; 7885 MW; 5069A5E6D3CC8F7 CRC64;

Query Match 2.2%; Score 8; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 20
MT2_NICGU STANDARD; PRT; 78 AA.
ID MT2_NICGU
AC Q40396;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metallothionein-like protein type 2.
OS Nicotiana glutinosa (Tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=35889;
RN [1]
RP SEQUENCE FROM N.A.
RA Choi D., Kim H.M., Yun H.K., Yi S.Y., Bok S.H.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Metallothioneins have a high content of cysteine
CC residues that bind various heavy metals.
CC -!- SIMILARITY: Belongs to the metallothionein superfamily. Family 15.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U46543; AAB0523.1; -.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
DR Metal-binding; Metal-thiolate-cluster.
SQ SEQUENCE 78 AA; 7869 MW; 8B78CDCFABD4A809 CRC64;

Query Match 2.2%; Score 8; DB 1; Length 78;

```

Best Local Similarity 100.0%; Pred. No. 9.8; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 21

Q93WM3 ID Q93WM3 PRELIMINARY; PRT; 78 AA.
AC Q93WM3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Metallothionein-like protein type 2.
OS Narcissus pseudonarcissus (Daffodil).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OC Narcissus.
ON NCBI_TaxID=39639;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=seencing tepals of 4-day old flowers;
RA Hunter D.A., Steele B.C., Reid M.S.;
RT Identification of genes associated with perianth senescence in
RL Plant Sci. 163:13-21(2002).
DR EMBL; AF420017; AAL16908.1;
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 78 AA; 7708 MW; 149B73425AEDB321 CRC64;

Query Match 2.2%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.8; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 22

Q94G67 ID Q94G67 PRELIMINARY; PRT; 78 AA.
AC Q94G67
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Metallothionein.
OS Amaranthus cruentus (Purple amaranth).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Amaranthus.
ON NCBI_TaxID=117272;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu F.-X., Sun M.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF268027; AAK57884.1;
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 78 AA; 7772 MW; 9CA27DBA2B2992C CRC64;

Query Match 2.2%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.8; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309

Db 4 CGGNCGCG 11

RESULT 23

Q6L8H8 ID Q6L8H8 PRELIMINARY; PRT; 78 AA.
AC Q6L8H8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Metallothionein 2.
OS Codonopsis lanceolata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Asterales; Campanulaceae; Codonopsis.
ON NCBI_TaxID=103999;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Branch;
RA In J.G., Yang D.C., Lee B.S.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB126057; BAD18924.1;
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 78 AA; 7826 MW; F8F087DC825F39B6 CRC64;

Query Match 2.2%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.8; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 24

Q6PML3 ID Q6PML3 PRELIMINARY; PRT; 78 AA.
AC Q6PML3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Metallothionein 2b.
GN Name=MT2b;
OS Populus balsamifera subsp. trichocarpa x Populus deltoides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Salicaceae; Populus.
ON NCBI_TaxID=3695;
RN [1]
RP SEQUENCE FROM N.A.
RA Kohler A., Blaudez D., Chalot M., Martin P.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY594298; AAT02525.1;
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 78 AA; 7901 MW; B43DECB278B82ADD CRC64;

Query Match 2.2%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.8; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 25

```

Q8GTD0
ID Q8GTD0 PRELIMINARY; PRT; 78 AA.
AC Q8GTD0;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Metallothioneine type2.
GN Name=mt2a;
OS Hordeum vulgare var. distichum (Two-rowed barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=112509;
RN [1]_TaxID=112509;
RP SEQUENCE FROM N.A.
RC TISSUE=Primary leaf;
RA Heise J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ511345; CAD54079.1; -.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
SQ SEQUENCE 78 AA; 7312 MW; 47498C0125352A3B CRC64;

Query Match 2.2%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGG 309
Db 4 CGGNCGG 11
|||||
|||||

```

Search completed: November 10, 2005, 09:46:49
 Job time : 174 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:20:26 ; Search time 54.2774 Seconds
(without alignments)
805.195 Million cell updates/sec

Title: US-10-606-055-2_COPY_258_370

Perfect score: 631

Sequence: 1 VLDRLNDKAKRYSCPRNY.....DIQLDHERCDCICSSRPPR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	123	7	Adk68116 Novel NOV
2	631	100.0	123	8	Adr49105 Human NOV
3	631	100.0	132	4	Aau00699 Human FCT
4	631	100.0	132	5	Abb79644 Human FCT
5	631	100.0	132	5	Abg78503 Human FCT
6	631	100.0	132	7	Adk68112 Novel NOV
7	631	100.0	132	8	Adm57645 Human FCT
8	631	100.0	132	8	Adr49101 Human NOV
9	631	100.0	152	4	Abb11697 Human nov
10	631	100.0	154	4	Aau00702 Human FCT
11	631	100.0	154	5	Abb79647 Human FCT
12	631	100.0	154	8	Adm57651 Human FCT
13	631	100.0	302	6	Abu72441 ZVEGF4-re
14	631	100.0	302	8	Adj32807 Fusion pr
15	631	100.0	316	6	Abu72442 ZVEGF4-re
16	631	100.0	316	8	Adj32808 Fusion pr
17	631	100.0	317	6	Abg75790 Human gro
18	631	100.0	322	3	Aay71129 Human pla
19	631	100.0	347	7	Adk68120 Novel NOV
20	631	100.0	347	8	Adr49109 Human NOV
21	631	100.0	358	5	Aae15852 Human mat
22	631	100.0	364	4	Aau12264 Human PRO
23	631	100.0	364	5	Aae15820 Human LP8
24	631	100.0	364	5	Abb84973 Human PRO
25	631	100.0	364	5	Abb95579 Human ang

26	631	100.0	364	6	ABO17708	Abol17708	Novel	hum
27	631	100.0	364	6	ABU80962	Abu80962	Human	PRO
28	631	100.0	364	6	ABU66662	Abu66662	Human	PRO
29	631	100.0	364	6	ABU59743	Abu59743	Novel	sec
30	631	100.0	364	6	ABO24933	Abol24933	Human	sec
31	631	100.0	364	6	ABU66938	Abu66938	Human	sec
32	631	100.0	364	6	ADA45705	Ada45705	Novel	hum
33	631	100.0	364	6	ADA76136	Ada76136	Human	PRO
34	631	100.0	364	6	ADA18786	Ada18786	Human	PRO
35	631	100.0	364	6	ADA61409	Ada61409	Homo sapi	
36	631	100.0	364	6	ADB19194	Adb19194	Novel	hum
37	631	100.0	364	6	ADB27735	Adb27735	Human	PRO
38	631	100.0	364	6	ADA86214	Ada86214	Novel	hum
39	631	100.0	364	6	ADB15778	Adb15778	Human	PRO
40	631	100.0	364	6	ADA47564	Ada47564	Human	PRO
41	631	100.0	364	6	ADA67359	Ada67359	Human	PRO
42	631	100.0	364	6	ADB30366	Adb30366	Human	PRO
43	631	100.0	364	6	ADA85662	Ada85662	Novel	hum
44	631	100.0	364	6	ADA96874	Ada96874	Human	PRO
45	631	100.0	364	6	ADA79178	Ada79178	Human	PRO
46	631	100.0	364	6	ADA87317	Ada87317	Novel	hum
47	631	100.0	364	6	ADB16519	Adb16519	Human	PRO
48	631	100.0	364	6	ADA91611	Ada91611	Novel	hum
49	631	100.0	364	6	ADB14674	Adb14674	Human	PRO
50	631	100.0	364	6	ADB18635	Adb18635	Novel	hum
51	631	100.0	364	6	ADA93850	Ada93850	Human	PRO
52	631	100.0	364	6	ADB19746	Adb19746	Novel	hum
53	631	100.0	364	6	ADB13058	Adb13058	Human	PRO
54	631	100.0	364	6	ABO43241	Abol43241	Novel	hum
55	631	100.0	364	6	ADA74312	Ada74312	Human	PRO
56	631	100.0	364	6	ADB24545	Adb24545	Human	PRO
57	631	100.0	364	6	ADA82069	Ada82069	Human	PRO
58	631	100.0	364	6	ADA75032	Ada75032	Human	PRO
59	631	100.0	364	6	ADA85110	Ada85110	Novel	hum
60	631	100.0	364	6	ADA84558	Ada84558	Novel	hum
61	631	100.0	364	6	ADB29814	Adb29814	Human	PRO
62	631	100.0	364	6	ADA80342	Ada80342	Human	PRO
63	631	100.0	364	6	ADA75584	Ada75584	Human	PRO
64	631	100.0	364	6	ADA46809	Ada46809	Human	PRO
65	631	100.0	364	6	ADB25105	Adb25105	Human	PRO
66	631	100.0	364	6	ADA93281	Ada93281	Human	PRO
67	631	100.0	364	6	ADB26631	Adb26631	Human	PRO
68	631	100.0	364	6	ADB30918	Adb30918	Human	PRO
69	631	100.0	364	6	ADA60846	Ada60846	Homo sapi	
70	631	100.0	364	6	ADB23993	Adb23993	Human	PRO
71	631	100.0	364	6	ADA96322	Ada96322	Human	PRO
72	631	100.0	364	6	ADA80894	Ada80894	Human	PRO
73	631	100.0	364	6	ADA95770	Ada95770	Human	PRO
74	631	100.0	364	6	ADB26079	Adb26079	Human	PRO
75	631	100.0	364	6	ADB21564	Adb21564	Novel	hum
76	631	100.0	364	7	ADA77343	Ada77343	Human	PRO
77	631	100.0	364	7	ADB18083	Adb18083	Human	PRO
78	631	100.0	364	7	ADA86766	Ada86766	Novel	hum
79	631	100.0	364	7	ADA87869	Ada87869	Novel	hum
80	631	100.0	364	7	ADA46257	Ada46257	Novel	hum
81	631	100.0	364	7	ADB28287	Adb28287	Human	PRO
82	631	100.0	364	7	ADB28839	Adb28839	Human	PRO
83	631	100.0	364	7	ADA76791	Ada76791	Human	PRO
84	631	100.0	364	7	ADA88421	Ada88421	Novel	hum
85	631	100.0	364	7	ADA97426	Ada97426	Human	PRO
86	631	100.0	364	7	ADB27183	Adb27183	Human	PRO
87	631	100.0	364	7	ADB22116	Adb22116	Novel	hum
88	631	100.0	364	7	ADA66807	Ada66807	Human	PRO
89	631	100.0	364	7	ADB22668	Adb22668	Human	PRO
90	631	100.0	364	7	ADB23441	Adb23441	Human	PRO
91	631	100.0	364	7	ADA92163	Ada92163	Novel	hum
92	631	100.0	364	7	ADB15226	Adb15226	Human	PRO
93	631	100.0	364	7	ADB38478	Adb38478	Novel	hum
94	631	100.0	364	7	ADB37926	Adb37926	Novel	hum
95	631	100.0	364	7	ADB66398	Adb66398	Novel	hum
96	631	100.0	364	7	ADB89478	Adb89478	Human	PRO
97	631	100.0	364	7	ADB90210	Adb90210	Human	PRO
98	631	100.0	364	7	ADB39311	Adb39311	Novel	hum

99 631 100.0 364 7 ADB46934 Novel hum
100 631 100.0 364 7 ADB86541 Human PRO

ALIGNMENTS

RESULT 1
ADK68116
ID ADK68116 standard; protein; 123 AA.
XX
AC ADK68116;
XX
DT 06-MAY-2004 (first entry)
XX
DE Novel NOVX protein #21.
XX
KW anti-diabetic; anorectic; cardiant; hypotensive; anti-arteriosclerotic;
KW anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
KW neuroprotective; anti-parkinsonian; anticonvulsant; osteopathic;
KW anti-arthritic; anti-inflammatory; dermatological; antiasthmatic;
KW anti-leptic; gene therapy; metabolic disorder; diabetes; obesity;
KW infectious disease; anorexia; cancer; cardiovascular disease;
KW hypertension; atherosclerosis; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
KW osteoarthritis; hematopoietic disorders; inflammatory skin disorder;
KW asthma; dyslipidemia; neurogenesis; cell differentiation;
KW cell proliferation; hematopoiesis; wound healing; angiogenesis;
KW chromosome mapping; pharmacogenomic.
XX
OS Homo sapiens.
XX
PN WO2003085124-A2.
XX
PD 16-OCT-2003.
XX
PF 01-APR-2003; 2003WO-US009775.
XX
PR 01-APR-2002; 2002US-0369065P.
PR 05-APR-2002; 2002US-0370279P.
PR 05-APR-2002; 2002US-0370359P.
PR 08-APR-2002; 2002US-0370969P.
PR 12-APR-2002; 2002US-0372019P.
PR 22-APR-2002; 2002US-0374379P.
PR 15-MAY-2002; 2002US-0380973P.
PR 30-MAY-2002; 2002US-0384297P.
PR 30-MAY-2002; 2002US-0384329P.
PR 17-JUN-2002; 2002US-0389729P.
PR 13-AUG-2002; 2002US-0403491P.
PR 15-AUG-2002; 2002US-0403748P.
PR 31-MAR-2003; 2003US-00403142.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsbrook JP, Bento P, Boldog FL, Burgess CE, Casman SJ;
PI Crabtree-Bokor JR, Edinger SR, Ellerman K, Fernandes ER, Gerlach VL;
PI Grosse WM, Gunther E, Guev VY, Heyes MP, Lepley DM, Li L;
PI MacDougall JR, Malyankar UM, Millet I, Patturajan M, Peyman JA;
PI Rastelli L, Rieger DK, Shenoy SG, Shinkets RD, Smithson G, Stone DJ;
PI Vernet CAM, Voss EZ;
XX
XX WPI; 2003-812730/76.
XX N-PSDB; ADK68115.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
XX Claim 1; SEQ ID NO 42; 323pp; English.
PS
XX The invention relates to novel NOVX protein and their encoding DNA's,
XX mature forms of the proteins or sequences that are at least 95% identical

CC to, or having one or more conservative amino acid substitutions in, the
CC proteins. The polypeptides, nucleic acid molecules and antibodies are
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such as metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), hematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidemias. The nucleic acids and polypeptides may
CC also be used as targets for the identification of small molecules that
CC modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC corresponds to one of the NOVX proteins of the invention.

XX Sequence 123 AA;

Query Match 100.0%; Score 631; DB 7; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.2e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VDLRLNDNDKAKRYSCPTPNYSVNIRELKLNVVFFPRCLLVQRCGCGGVNWRSC 60
Db 11 VDLRLNDNDKAKRYSCPTPNYSVNIRELKLNVVFFPRCLLVQRCGCGGVNWRSC 70
Qy 61 CNSGKTVKKYHEVLQEPGHIKRGRAKTALVDIQLDHHRCDCICSSRP 113
Db 71 CNSGKTVKKYHEVLQEPGHIKRGRAKTALVDIQLDHHRCDCICSSRP 123

RESULT 2

ADR49105
ID ADR49105 standard; protein; 123 AA.
XX
AC ADR49105;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human NOV4c protein.
XX
KW NOVX; human; cardiomyopathy; atherosclerosis; hypertension,
KW pulmonary stenosis; obesity; prostate cancer; diabetes; haemophilia;
KW skin disorder; graft versus host disease; AIDS; asthma; lupus;
KW Crohn's disease; inflammatory bowel disease; ulcerative colitis;
KW multiple sclerosis; infectious disease; anorexia; Alzheimer's disease;
KW Parkinson's disease; NOV4c.
XX
OS Homo sapiens.
XX
XX US20041622336-A1.
PN
XX
XX 19-AUG-2004.
PD
XX
XX 31-MAR-2003; 2003US-00403142.
XX
XX 01-APR-2002; 2002US-0369065P.
PR
XX 05-APR-2002; 2002US-0370279P.
PR
XX 05-APR-2002; 2002US-0370359P.
PR
XX 05-APR-2002; 2002US-0370381P.
PR
XX 08-APR-2002; 2002US-0370969P.
PR
XX 12-APR-2002; 2002US-0372019P.
PR
XX 22-APR-2002; 2002US-0374379P.
PR
XX 15-MAY-2002; 2002US-0380973P.
PR
XX 30-MAY-2002; 2002US-0384297P.
PR
XX 30-MAY-2002; 2002US-0384329P.
PR
XX 17-JUN-2002; 2002US-0389729P.
PR
XX 13-AUG-2002; 2002US-0403491P.

PR 15-AUG-2002; 2002US-0403748P.
XX (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASN/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELJERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
XX
XX Alsobrook J, Bento P, Boldog F, Burgess C, Casman S, Bokor JC;
PI Edinger SR, Ellerman K, Fernandes E, Gerlach V, Grosse W, Gunther E;
PI Gusev V, Heyes M, Lepley D, Li L, MacDougall JR, Malyankar UM;
PI Millet I, Patturajan M, Peyman JA, Rastelli L, Rieger D, Shenoy S;
PI Shinkets R, Smithson G, Stone D, Vernet C, Voss E;
XX
XX WPI: 2004-603580/58.
DR N-PSDB; ADR49104.
XX
XX New isolated polypeptides and nucleic acids, useful for treating or
PT preventing, e.g. cardiomyopathy, atherosclerosis, hypertension, obesity,
PT prostate cancer, diabetes, hemophilia, AIDS, inflammatory bowel disease,
PT or infectious disease.
XX
XX Claim 1; SEQ ID NO 42; 206pp; English.
XX
XX This invention describes novel human NOVX polypeptides and the
CC polynucleotides encoding them. The therapeutic is useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease selected from pathology associated with the polypeptide.
CC Diseases include cardiomyopathy, atherosclerosis, hypertension, pulmonary
CC stenosis, obesity, prostate cancer, diabetes, hemophilia, skin
CC disorders, graft versus host disease, AIDS, asthma, lupus, Crohn's
CC disease, inflammatory bowel disease, ulcerative colitis, multiple
CC sclerosis, infectious disease, anorexia, Alzheimer's disease, or
CC Parkinson's disease. They are also useful in detection assays, chromosome
CC mapping, or tissue typing. This sequence represents the human NOV4c
XX protein.
XX
SQ Sequence 123 AA;
Query Match 100.0%; Score 631; DB 8; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.2e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLDRLNDKAYSCYTPRNVNIREELKLVNVPFRCLLVQRCGNCGGTNNRST 60
DB 11 VLDRLNDKAYSCYTPRNVNIREELKLVNVPFRCLLVQRCGNCGGTNNRST 70
QY 61 CNSGKTVKKYHEVLQPEPGHIKRRGAKTMALVDIOLDHHERCDICSSRPPR 113
|||||

Db 71 CNSGKTVKKYHEVLQPEPGHIKRRGAKTMALVDIOLDHHERCDICSSRPPR 123
RESULT 3
AAU00699
ID AAU00699 standard; protein; 132 AA.
XX AC AAU00699;
XX 07-SEP-2001 (first entry)
XX Human FCTR2 protein present in clone 30664188.0.331.
XX
XX Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;
KW VEGF-E; platelet derived growth factor; PDGF; FCTR; hyperplasia; cancer;
KW neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;
KW fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;
KW dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;
KW inflammatory disorder; graft versus host disease; coagulation;
KW haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;
KW multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
KW peripheral neuropathy; acute brain injury.
XX
XX Homo sapiens.
XX
XX WO200125437-A2.
XX PD 12-APR-2001. possible
XX PF 06-OCT-2000; 2000WO-US027671.
XX
XX 07-OCT-1999; 99US-0158083P.
PR 13-OCT-1999; 99US-0159231P.
PR 04-JAN-2000; 2000US-0174485P.
PR 03-MAR-2000; 2000US-0186707P.
PR 10-MAR-2000; 2000US-0189250P.
PR 08-AUG-2000; 2000US-0223879P.
PR 12-SEP-2000; 2000US-00662783.
PR 20-SEP-2000; 2000US-0234082P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
PI Jeffers M;
XX
XX WPI: 2001-316172/33.
DR N-PSDB; AAS04493.
XX
XX Novel growth factor polypeptides termed as FCTR polypeptides, useful for
PT treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
PT wound healing and neuronal disorders.
XX
XX Claim 1; Page 14-15; 171pp; English.
XX
XX The sequence represents a protein related to bone morphogenetic protein-1
CC (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived
CC growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1,
CC VEGF-E and PDGF are referred to as FCTR polypeptides and nucleic acids.
CC FCTR proteins are useful for treating or preventing a disorder
CC associated with aberrant expression, aberrant processing, or aberrant
CC physiological interactions of the protein in a mammal, where the
CC disorder is characterised by insufficient or ineffective growth of a cell
CC or a tissue, e.g. hyperplasia or neoplasia. The peptides and their
CC associated nucleic acids are useful for both promoting and inhibiting
CC growth of cells and tissues and in treatment of cancer, anaemia,
CC leukopenia, baldness, for treating cardiovascular and fibrotic disorders,
CC diabetic ulcers, obesity, infectious diseases, hyperproliferative and
CC dysproliferative disorders, neurodegenerative disorders, osteoarthritis,
CC inflammatory disorders, Graft versus host disease, coagulation disorders
CC such as haemophilia, and neural disorders including Parkinson's disease,
CC Alzheimer's disease, multiple sclerosis, Huntington's disease.
CC Amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
CC and epilepsy

RESULT 6
ADK68112
ID ADK68112 standard; protein; 132 AA.
XX
AC ADK68112;
XX
DT 06-MAY-2004 (first entry)
XX
DE Novel NOVX protein #19.
XX
KW antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic;
KW anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
KW neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
KW antiarthritic; antiinflammatory; dermatological; antiasthmatic;
KW antilipemic; gene therapy; metabolic disorder; diabetes; obesity;
KW infectious disease; anorexia; cancer; cardiovascular disease;
KW hypertension; atherosclerosis; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
KW osteoarthritis; hematopoietic disorders; inflammatory skin disorder;
KW asthma; dyalipidemia; neurogenesis; cell differentiation;
KW cell proliferation; hematopoiesis; wound healing; angiogenesis;
KW chromosome mapping; pharmacogenomic.
XX
OS Homo sapiens.
XX
PN WO2003085124-A2.
XX
PD 16-OCT-2003.
XX
PF 01-APR-2003; 2003WO-US009775.
XX
PR 01-APR-2002; 2002US-0369065P.
PR 05-APR-2002; 2002US-0370279P.
PR 05-APR-2002; 2002US-0370359P.
PR 08-APR-2002; 2002US-0370969P.
PR 12-APR-2002; 2002US-0372019P.
PR 22-APR-2002; 2002US-0374379P.
PR 15-MAY-2002; 2002US-0380973P.
PR 30-MAY-2002; 2002US-0384297P.
PR 30-MAY-2002; 2002US-0384329P.
PR 17-JUN-2002; 2002US-0389729P.
PR 13-AUG-2002; 2002US-0403491P.
PR 15-AUG-2002; 2002US-0403748P.
PR 31-MAR-2003; 2003US-00403142.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Bento P, Boldog FL, Burgess CE, Casman SJ;
PI Crabtree-Bokor JR, Edinger SR, Ellerman K, Fernandes ER, Gerlach VL;
PI Grose WM, Gunther E, Gusev VV, Heyes MP, Lepley DM, Li L;
PI Macdougall JR, Malyankar UM, Millet I, Patturajan M, Peyman JA;
PI Rastelli L, Rieger DK, Shenoy SG, Shinkets RD, Smithson G, Stone DJ;
PI Vernet CAM, Voss EZ;
XX
WPI; 2003-812730/76.
DR N-PSDB; ADK68111.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
XX Claim 1; SEQ ID NO 38; 323pp; English.
XX
XX The invention relates to novel NOVX protein and their encoding DNA's,
CC mature forms of the proteins or sequences that are at least 95% identical
CC to, or having one or more conservative amino acid substitutions in, the
CC proteins. The polypeptides, nucleic acid molecules and antibodies are
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such metabolic disorders,

CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), hematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidemias. The nucleic acids and polypeptides may
CC also be used as targets for the identification of small molecules that
CC modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC corresponds to one of the NOVX proteins of the invention.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 631; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.5e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLDRLNDDAKRYSCYTPRNSVNIREEELKLANVFFPRCLLVQRCGNGCGGTVNRSC 60
DB 20 VLDRLNDDAKRYSCYTPRNSVNIREEELKLANVFFPRCLLVQRCGNGCGGTVNRSC 79
QY 61 CNSGKTVKKYHEVLQFEPGHKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
DB 80 CNSGKTVKKYHEVLQFEPGHKRRGRKTMALVDIQLDHHRCDCICSSRPPR 132
RESULT 7
ADM57645
ID ADM57645 standard; protein; 132 AA.
XX
AC ADM57645;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human FCTR2 protein.
XX
KW Fibroblast growth factor-CX; FGF-CX; FCTR; inflammatory bowel disease;
KW inflammation; Crohn's disease; gene therapy;
KW platelet-derived growth factor; PDGPD; human.
XX
OS Homo sapiens.
XX
PN US2004006015-A1.
XX
PD 08-JAN-2004.
XX
PF 16-DEC-2002; 2002US-00321962.
XX
PR 16-NOV-2001; 2001US-00011364.
PR 06-JUN-2002; 2002US-0386545P.
XX
PA (BOLD/) BOLD OG F L.
PA (BURG/) BURGESS C E.
PA (FEEN/) FERNANDES E R.
PA (JEFF/) JEFFERS M E.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (PETE/) PETERSON J.
PA (PRAY/) PRAYAGA S K.
PA (RITT/) RITTMAN B.
PA (SHIM/) SHIMKETS J B.
PA (SHIM/) SHIMKETS R A.
PA (YANG/) YANG M.
XX
Boldog FL, Burgess CE, Fernandes ER, Jeffers ME, Larochelle WJ;
PI Lichenstein HS, Peterson J, Prayaga SK, Rittman B, Shinkets JB;
PI Shinkets RA, Yang M;
XX WPI; 2004-081737/08.
DR

DR N-PSDB; ADM57644.

XX Promoting the growth of a population of cells, useful for treating

PT inflammatory conditions, comprises contacting the at least one cell with

PT a composition comprising FGFCX and/or FCTRXX polypeptides.

XX

XX Claim 4; SEQ ID NO 6; 153pp; English.

XX

XX The present invention is based upon methods of treating inflammatory

CC conditions in the intestinal tract of mammals using fibroblast growth

CC factor (FGF)-CX and/or FCTRXX(undefined) polypeptides and their encoding

CC polynucleotides. The invention is useful for treating inflammatory

CC pathology such as inflammatory bowel disease, inflammatory condition

CC occurring in the colon or small intestine and Crohn's disease. The

CC invention is also useful in gene therapy. The present sequence is human

CC FCTRXX protein. The sequence is also referred as human platelet-derived

CC growth factor D (PDGFD) protein.

XX

XX Sequence 132 AA;

Query Match 100.0%; Score 631; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 3.5e-62;

Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDDAKRYCTPRNYSWNIREELKLANVFFPRCLLVQRCGCGGTVNWRSCT 60

Db 20 VDLRLNDDAKRYCTPRNYSWNIREELKLANVFFPRCLLVQRCGCGGTVNWRSCT 79

QY 61 CNSGKTVKVYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113

Db 80 CNSGKTVKVYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 132

RESULT 8

ADR49101

ID ADR49101 standard; protein; 132 AA.

XX

AC ADR49101;

XX

DT 04-NOV-2004 (first entry)

XX

DE Human NOV4a protein.

XX

KW NOVX; human; cardiomyopathy; atherosclerosis; hypertension;

KW pulmonary stenosis; obesity; prostate cancer; diabetes; haemophilia;

KW skin disorder; graft versus host disease; AIDS; asthma; lupus;

KW Crohn's disease; inflammatory bowel disease; ulcerative colitis;

KW multiple sclerosis; infectious disease; anorexia; Alzheimer's disease;

KW Parkinson's disease; NOV4a.

XX

OS Homo sapiens.

XX

XX US2004162236-A1.

PN

XX

PD 19-AUG-2004.

XX

PF 31-MAR-2003; 2003US-00403142.

XX

PR 01-APR-2002; 2002US-0369065P.

PR 05-APR-2002; 2002US-0370279P.

PR 05-APR-2002; 2002US-0370359P.

PR 08-APR-2002; 2002US-0370381P.

PR 08-APR-2002; 2002US-0370969P.

PR 12-APR-2002; 2002US-0372019P.

PR 22-APR-2002; 2002US-0374379P.

PR 15-MAY-2002; 2002US-0380973P.

PR 30-MAY-2002; 2002US-0384297P.

PR 30-MAY-2002; 2002US-0384329P.

PR 17-JUN-2002; 2002US-0389729P.

PR 13-AUG-2002; 2002US-0403491P.

PR 15-AUG-2002; 2002US-0403748P.

XX

XX (ALSO/) ALSOBROOK J.

PA (BENT/) BENTO P.

PA (BOLD/) BOLDOG F.

PA (BURG/) BURGESS C.

PA (CASM/) CASMAN S.

PA (BOKO/) BOKOR J C.

PA (EDIN/) EDINGER S R.

PA (ELLE/) ELLERMAN K.

PA (FERN/) FERNANDES E.

PA (GERL/) GERLACH V.

PA (GROS/) GROSSE W.

PA (GUNT/) GUNTHER E.

PA (GUSE/) GUSEV V.

PA (HEYE/) HEYES M.

PA (LEPL/) LEPLEY D.

PA (LILL/) LI L.

PA (MACD/) MACDOUGALL J R.

PA (MALY/) MALYANKAR U M.

PA (MILL/) MILLET I.

PA (PAT/) PATTURAJAN M.

PA (PEYM/) PEYMAN J A.

PA (RAST/) RASTELLI L.

PA (RIEG/) RIEGER D.

PA (SHEN/) SHENOY S.

PA (SHIM/) SHIMKETS R.

PA (SMIT/) SMITHSON G.

PA (STON/) STONE D.

PA (VERN/) VERNET C.

PA (VOSS/) VOSS E.

XX

PI Alsebrook J, Bento P, Boldog F, Burgess C, Casman S, Bokor JC;

PI Edinger SR, Ellerman K, Fernandes E, Gerlach V, Grosse W, Gunther E;

PI Gusev V, Heyes M, Lepley D, Li L, Macdougall JR, Malyankar UM;

PI Millet I, Patturajan M, Peyman JA, Rastelli L, Rieger D, Shenoy S;

PI Shimkets R, Smithson G, Stone D, Vernet C, Voss E;

XX

DR WPI; 2004-603580/58.

DR N-PSDB; ADR49100.

XX

PT New isolated polypeptides and nucleic acids, useful for treating or

PT preventing, e.g. cardiomyopathy, atherosclerosis, hypertension, obesity,

PT prostate cancer, diabetes, hemophilia, AIDS, inflammatory bowel disease,

PT or infectious disease.

XX

PS Claim 1; SEQ ID NO 38; 206pp; English.

XX

CC This invention describes novel human NOVX polypeptides and the

CC polynucleotides encoding them. The therapeutic is useful in the

CC manufacture of a medicament for treating a syndrome associated with a

CC human disease selected from pathology associated with the polypeptide.

CC Diseases include cardiomyopathy, atherosclerosis, hypertension, pulmonary

CC stenosis, obesity, prostate cancer, diabetes, haemophilia, skin

CC disorders, graft versus host disease, AIDS, asthma, lupus, Crohn's

CC disease, inflammatory bowel disease, ulcerative colitis, multiple

CC sclerosis, infectious disease, anorexia, Alzheimer's disease, or

CC Parkinson's disease. They are also useful in detection assays, chromosome

CC mapping, or tissue typing. This sequence represents the human NOV4a

CC protein.

XX

XX Sequence 132 AA;

Query Match 100.0%; Score 631; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 3.5e-62;

Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDDAKRYCTPRNYSWNIREELKLANVFFPRCLLVQRCGCGGTVNWRSCT 60

Db 20 VDLRLNDDAKRYCTPRNYSWNIREELKLANVFFPRCLLVQRCGCGGTVNWRSCT 79

QY 61 CNSGKTVKVYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113

Db 80 CNSGKTVKVYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 132

RESULT 9

ABBI1697

ID ABB11697 standard; peptide; 152 AA.

XX AC ABB11697;

DT 11-JAN-2002 (first entry)

XX

XX Human novel protein, SEQ ID NO:2067.

DE

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;

XX haematopoiesis regulation; tissue growth; immunomodulator; activin;

KW inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;

KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;

KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

KW chronic inflammatory condition; proliferative retinopathy;

KW atherosclerosis; coronary heart disease; arterial ischaemia;

KW bone disorder; osteoporosis; vascular growth disorder;

KW tissue regeneration; wound healing; infection; immune disorder;

KW cell culture; drug screening; gene therapy; antiinflammatory;

KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;

KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;

KW antifungal; vulnery; antiulcer.

XX

XX Homo sapiens.

OS

XX WO200157188-A2.

PN

XX

XX 09-AUG-2001. *125437 A2*

PD

XX

XX 05-FEB-2001; 2001WO-US003800.

PF

XX

XX 03-FEB-2000; 2000US-00496914.

PR

XX 27-APR-2000; 2000US-00560875.

PR

XX (HYSE-) HYSEQ INC.

PA

XX

XX Tang YT, Liu C, Drmanac RT;

PI

XX WPI; 2001-457740/49.

PI

XX N-PSDB; ABA08941.

DR

XX

XX Human proteins and DNA encoding sequences useful for preventing, treating

PT

XX or ameliorating a medical condition in a mammalian subject e.g. arthritis

PT

XX and cancer.

XX

XX Claim 20; Page 229; 1963pp; English.

PS

XX

XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and

CC

XX sequences ABA08225-ABA09574 represent nucleic acids encoding them. The

CC

XX invention also relates to vectors and recombinant host cells comprising a

CC

XX nucleotide of the invention, methods of producing the novel polypeptides,

CC

XX antibodies against the polypeptides, methods of detecting the nucleotides

CC

XX or polypeptides in a sample, and methods of identifying compounds which

CC

XX bind to polypeptides of the invention. Although novel, many of the

CC

XX polypeptides of the invention have homology to known proteins, thereby

CC

XX giving an insight into their probable biological activities, and hence

CC

XX potential therapeutic applications. The polypeptides of the invention may

CC

XX have various activities, including cytokine, cell proliferation or cell

CC

XX differentiation activities; stem cell growth factor activity;

CC

XX haematopoiesis regulatory activity; tissue growth activity;

CC

XX immunomodulatory activity; activin- or inhibin-related activities;

CC

XX chemotactic or chemokinetic activities; haemostatic, thrombotic or

CC

XX thrombolytic activities; receptor or ligand activities; or may be

CC

XX involved in oncogenesis, cancer cell proliferation or metastasis.

CC

XX Depending on their biological activities, polypeptides and nucleotides of

CC

XX the invention are useful for preventing, treating or ameliorating medical

CC

XX conditions, e.g., by protein or gene therapy. Such conditions include

CC

XX cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC

XX disorders), chronic inflammatory conditions (e.g., asthma or arthritis),

CC

XX proliferative retinopathy, atherosclerosis, coronary heart disease,

CC

XX arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC

XX vascular growth. Polypeptides involved with tissue regeneration and

CC

XX

CC repair (or nucleic acids encoding them) may be used to promote wound

CC healing (e.g., of burns, incisions and ulcers), while those with

CC immunomodulatory activities may be used in the treatment of viral,

CC bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to

CC promote cell growth. For example, such polypeptides may be used to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC that can be used to augment or replace cells damaged by illness,

CC autoimmune disease or accidental damage. The polypeptides and nucleotides

CC may also be used in the diagnosis of the above conditions, and in drug

CC screening techniques. The present sequence represents a novel human

CC polypeptide of the invention

XX

SQ Sequence 152 AA;

Query Match 100.0%; Score 631; DB 4; Length 152;

Best Local Similarity 100.0%; Pred. No. 4, 1e-62;

Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 VDLRLNDDAKRYSCYPRNYSVINBELKLANVFFPRCLLVORCGNGCGGTNNRSCT 60

DB 40 VDLRLNDDAKRYSCYPRNYSVINBELKLANVFFPRCLLVORCGNGCGGTNNRSCT 99

QY 61 CNSGKTVKYYHEVLQEPFGHKKRGRKTMALVDIQLDHHRCDCICSSRPPR 113

DB 100 CNSGKTVKYYHEVLQEPFGHKKRGRKTMALVDIQLDHHRCDCICSSRPPR 152

RESULT 10

AAU00702

ID AAU00702 standard; protein; 154 AA.

XX AC AAU00702;

XX

DT 07-SEP-2001 (first entry)

XX

DE Human FCTR5 protein present in clone pCR2.1-S852_2B.

XX

XX Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;

KW VEGF-E; platelet derived growth factor; PDGF; FCTR5; hyperplasia; cancer;

KW neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;

KW fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;

KW dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;

KW inflammatory disorder; Graft versus host disease; coagulation;

KW haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;

KW multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;

KW peripheral neuropathy; acute brain injury.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Peptide 1..23 /note= "Signal peptide"

FT Protein 24..154 /note= "Mature FCTR5"

FT

XX WO200125437-A2.

XX

PD 12-APR-2001. *125437 A2*

XX

XX 06-OCT-2000; 2000WO-US027671.

XX

XX 07-OCT-1999; 99US-0158083P.

PR 13-OCT-1999; 99US-0159231P.

PR 03-JAN-2000; 2000US-0174485P.

PR 03-MAR-2000; 2000US-0186707P.

PR 10-MAR-2000; 2000US-0188250P.

PR 08-AUG-2000; 2000US-0223879P.

PR 12-SEP-2000; 2000US-00662783.

PR 20-SEP-2000; 2000US-0234082P.

XX

XX (CURA-) CURAGEN CORP.

XX

PI Shimkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
PI Jeffers M;
XX
DR WPI; 2001-316172/33.
DR N-PSDB; AAS04496.
XX
XX Novel growth factor polypeptides termed as FCTR5 polypeptides, useful for
PT treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
PT wound healing and neuronal disorders.
XX
XX
PS Claim 1; Page 19; 171pp; English.
XX
XX The sequence represents a protein related to bone morphogenetic protein-1
CC (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived
CC growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1,
CC VEGF-E and PDGF are referred to as FCTR5 peptides and nucleic acids.
CC FCTR5 proteins are useful for treating or preventing a disorder
CC associated with aberrant expression, aberrant processing, or aberrant
CC physiological interactions of the proteins in a mammal, where the
CC disorder is characterised by insufficient or ineffective growth of a cell
CC or a tissue, e.g. hyperplasia or neoplasia. The peptides and their
CC associated nucleic acids are useful for both promoting and inhibiting
CC growth of cells and tissues and in treatment of cancer, anaemia,
CC leukopenia, baldness, for treating cardiovascular and fibrotic disorders,
CC diabetic ulcers, obesity, infectious diseases, hyperproliferative and
CC dysproliferative disorders, neurodegenerative disorders, osteoarthritis,
CC inflammatory disorders, graft versus host disease, coagulation disorders
CC such as haemophilia, and neural disorders including Parkinson's disease,
CC Alzheimer's disease, multiple sclerosis, Huntington's disease,
CC amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
CC and epilepsy
XX
SQ Sequence 154 AA;
Query Match 100.0%; Score 631; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 4.1e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDLRLNDKAKRYCTPRNYSVNIREELKLANVFFPRLCLLVQRCGCGGTNNRSCT 60
DB 42 VDLRLNDKAKRYCTPRNYSVNIREELKLANVFFPRLCLLVQRCGCGGTNNRSCT 101
QY 61 CNSGKTVKXKHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRRPR 113
DB 102 CNSGKTVKXKHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRRPR 154
RESULT 11
ABB79647
XX
XX ABB79647 standard; protein; 154 AA.
AC ABB79647;
XX
XX 21-OCT-2002 (first entry)
DT
XX
XX Human FCTR5 (platelet derived growth factor D).
XX
XX FCTR5; platelet derived growth factor D; PDGFD; human; Crohn's disease;
KW inflammatory bowel disease; gene therapy; antiinflammatory; vulnerary;
KW cystostatic; cardiovascular.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..23
FT Peptide /label= Signal_peptide
FT Protein 24..154
FT /label= Mature_protein
XX
XX WO200258716-A2.
PN
XX
XX 01-AUG-2002.
PD
XX
XX

PF 06-NOV-2001; 2001WO-US043846.
XX
PR 06-NOV-2000; 2000US-0246206P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Jeffers M, Shimkets RA, Pravaga S, Boldog FL, Yang M, Burgess CE;
PI Fernandes ER, Rittman B, Shimkets JB, Larochele WJ, Lichenstein HS;
XX
DR WPI; 2002-599742/64.
DR N-PSDB; AEN84528.
XX
XX Treating, delaying the onset of, or ameliorating an inflammatory
PT pathology (e.g. inflammatory bowel disease or Crohn's disease) by
PT administering to the subject fibroblast growth factors or a combination
PT of growth factors.
XX
PS Claim 5; Page 26; 196pp; English.
XX
XX The present sequence is the protein sequence of FCTR5, also referred to
CC as platelet derived growth factor D (PDGFD) or human PDGFD. FCTR5 is a
CC splice variant of FCTR1 (see ABB79643). It contains a characteristic
CC signal peptide, PDGF domain and N-glycosylation site. Human FCTR5 is most
CC closely related to human PDGF C, B and A. The invention provides FQFCX
CC and FCTR5 growth factors, polypeptides and variants, and polynucleotides
CC encoding them, and methods of using these to treat, delay the onset of,
CC or ameliorate, an inflammatory pathology, especially inflammatory bowel
CC disease, a disease that occurs in the colon or small intestine, or
CC Crohn's disease (all claimed). The FQFCX and FCTR5 polypeptides and
CC polynucleotides are also useful for treating growth and proliferative
CC diseases such as cancer, angiogenesis, collagen formation, fibrotic and
CC cardiovascular diseases or diabetic ulcers, and in wound healing. They
CC can be used in screening and detection methods, chromosome mapping,
CC tissue typing, predictive medicine, diagnostic assays, prognostic assays,
CC and pharmacogenomics
XX
SQ Sequence 154 AA;
Query Match 100.0%; Score 631; DB 5; Length 154;
Best Local Similarity 100.0%; Pred. No. 4.1e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDLRLNDKAKRYCTPRNYSVNIREELKLANVFFPRLCLLVQRCGCGGTNNRSCT 60
DB 42 VDLRLNDKAKRYCTPRNYSVNIREELKLANVFFPRLCLLVQRCGCGGTNNRSCT 101
QY 61 CNSGKTVKXKHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRRPR 113
DB 102 CNSGKTVKXKHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRRPR 154
RESULT 12
ADM57651
ID ADM57651 standard; protein; 154 AA.
XX
XX ADM57651;
AC
XX
XX 03-JUN-2004 (first entry)
DT
XX
XX Human FCTR5 protein.
DE
XX
KW Fibroblast growth factor-CX; FGF-CX; FCTR5; inflammatory bowel disease;
KW inflammation; Crohn's disease; gene therapy;
KW platelet-derived growth factor; PDGFD; human.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..23
FT Peptide /label= Signal_peptide
FT Protein 24..154
FT /note= "Human mature FCTR5 protein"
XX
XX

PN US2004006015-A1.
XX
PD 09-JAN-2004.
PF
PF 16-DEC-2002; 2002US-00321962.
XX
PR 16-NOV-2001; 2001US-00011364.
PR 06-JUN-2002; 2002US-0386545P.
XX
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (FERN/) FERNANDES E R. I
PA (JEFF/) JEFFERS M E.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (PETE/) PETERSON J.
PA (PRAY/) PRAYAGA S K.
PA (RITT/) RITTMAN B.
PA (SHIM/) SHIMKETS J B.
PA (SHIM/) SHIMKETS R A.
PA (YANG/) YANG M.
XX
XX Boldog FL, Burgess CE, Fernandes ER, Jeffers ME, Larochelle WJ;
PI Lichenstein HS, Peterson J, Prayaga SK, Rittman B, Shimkets JB;
PI Shimkets RA, Yang M;
XX
XX WPI; 2004-081737/08.
DR N-PSDB; ADM57650.
XX
XX Promoting the growth of a population of cells, useful for treating
PT inflammatory conditions, comprises contacting the at least one cell with
PT a composition comprising FGFCX and/or FCTR polypeptides.
XX
XX Claim 4; SEQ ID NO 12; 153pp; English.
XX
XX The present invention is based upon methods of treating inflammatory
CC conditions in the intestinal tract of mammals using fibroblast growth
CC factor (FGF)-CX and/or FCTR(undefined) polypeptides and their encoding
CC polynucleotides. The invention is useful for treating inflammatory
CC pathology such as inflammatory bowel disease, inflammatory condition
CC occurring in the colon or small intestine and Crohn's disease. The
CC invention is also useful in gene therapy. The present sequence is human
CC FCTR protein. The sequence is also referred as human platelet-derived
CC growth factor D (PDGFD) cDNA.
XX
XX Sequence 154 AA;
SQ
Query Match 100.0%; Score 631; DB 8; Length 154;
Best Local Similarity 100.0%; Pred. No. 4.1e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDLRLNDADAKYSCCTPRNYSVNIREELKLANVVFPRCLLVQRCGNGCGGTNNRSCT 60
DB 42 VDLRLNDADAKYSCCTPRNYSVNIREELKLANVVFPRCLLVQRCGNGCGGTNNRSCT 101
QY 61 CNSGKTVKKYHEVLQEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPPR 113
DB 102 CNSGKTVKKYHEVLQEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPPR 154
RESULT 13
ABU72441
ID ABU72441 standard; protein; 302 AA.
XX
XX ABU72441;
XX
XX 16-JUN-2003 (first entry)
XX
XX ZVEGF4-related fusion protein #1.
XX
XX Growth factor homologue; ZVEGF4; proliferation; differentiation;
KW migration; mesenchymal cell; cell surface semaphorin; neuropilin;
KW neurite growth; cardiovascular development; limb development;

KW cartilage development; T-cell; B-cell; rheumatoid arthritis; cancer;
KW autoimmune disease; inflammation; retinopathy; haemangioma;
KW ischaemic event; neuropathy; acute nerve damage; stroke;
KW central nervous system disease; peripheral nervous system disease.
XX
OS Unidentified.
XX
XX US6495668-B1.
XX
XX 17-DEC-2002.
XX
XX 03-MAY-2000; 2000US-00564595.
XX
XX 03-MAY-1999; 99US-0132250P.
PR 10-NOV-1999; 99US-0164463P.
PR 04-FEB-2000; 2000US-0180169P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
PI
XX WPI; 2003-352153/33.
XX
XX Isolated growth factor analogue ZVEGF4 proteins for pharmaceutical
PT composition as, e.g. therapeutic agents, diagnostic agents, and research
PT tools and reagents, includes polypeptides from amino acid residues.
XX
XX Claim 14; Col 107-110; 67pp; English.
XX
XX The invention relates to an isolated protein comprising a first
CC polypeptide disulphide-bonded to a second polypeptide. The first and
CC second polypeptides are from 113-138 amino acid residues and comprises
CC 258-370 amino acid residues of human growth factor homologue ZVEGF4. The
CC protein stimulates proliferation, differentiation, or migration of
CC mesenchymal cells and may modulate activities mediated by cell surface
CC semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-
CC semaphorin interactions which may be of use in neurite growth,
CC cardiovascular development, cartilage and limb development, T- and B-cell
CC functions as well as treating rheumatoid arthritis, various forms of
CC cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas,
CC ischaemic events, neuropathies, acute nerve damage, central nervous
CC system diseases and peripheral nervous system diseases including stroke.
CC The isolated protein is also used for a pharmaceutical composition as
CC therapeutic agents, diagnostic agents, and research tools and reagents.
CC It can be used in the study and regulation of cell and tissue
CC development, as components of cell culture media. The proteins can form
CC homomultimers or heteromultimers that act on tissues to control organ
CC development by modulating cell proliferation, migration, differentiation,
CC or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3
CC -23.1. The present sequence represents a ZVEGF4-related fusion protein
CC (claimed but not further defined in the specification)
XX
XX Sequence 302 AA;
SQ
Query Match 100.0%; Score 631; DB 6; Length 302;
Best Local Similarity 100.0%; Pred. No. 8.8e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDLRLNDADAKYSCCTPRNYSVNIREELKLANVVFPRCLLVQRCGNGCGGTNNRSCT 60
DB 190 VDLRLNDADAKYSCCTPRNYSVNIREELKLANVVFPRCLLVQRCGNGCGGTNNRSCT 249
QY 61 CNSGKTVKKYHEVLQEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPPR 113
DB 250 CNSGKTVKKYHEVLQEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPPR 302
RESULT 14
ADJ32807
ID ADJ32807 standard; protein; 302 AA.
XX
XX ADJ32807;
AC
XX

DT 15-APR-2004 (first entry)
DE Fusion protein #used in the invention.
XX
XX Growth factor homologue; zvegfg4; skin wound; venous stasis; ulcer;
KW fracture repair; skin grafting; neovascularisation;
KW female reproductive tract disorder; bleeding; gastrointestinal tract;
KW liver damage; hepatic chronic passive congestion; CPC;
KW central haemorrhagic necrosis; CHN; neurite growth; neuropathy;
KW neurodegenerative disease; multiple sclerosis; Alzheimer's disease;
KW Parkinson's disease; cell proliferation; cancer; gene therapy.
XX
XX Unidentified.
OS
XX
XX US2004002140-A1.
PN
XX
XX 01-JAN-2004.
PD
XX
XX 06-JUN-2001; 2001US-00876813.
PF
XX
XX 03-MAY-1999; 99US-0132250P.
PR
XX
XX 10-NOV-1999; 99US-0164463P.
PR
XX
XX 04-FEB-2000; 2000US-0180169P.
PR
XX
XX 03-MAY-2000; 2000US-00564595.
XX
XX (GILB/) GILBERT T.
PA (HART/) HART C.E.
PA (SHEP/) SHEPPARD P.O.
PA (GILB/) GILBERTSON D.G.
XX
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
PI
XX
XX WPI; 2004-070738/07.
DR
XX
XX New zvegfg4 polypeptides and nucleic acids, useful for diagnosing or
PT treating cell loss or abnormal cell proliferation, e.g. cancer, treating
PT full-thickness skin wounds or treating female reproductive tract
PT disorders.
XX
XX Disclosure; SEQ ID NO 54; 73pp; English.
XX
XX The invention relates to growth factor homologue zvegfg4, its
CC corresponding nucleic acid and methods of using them. The sequences of
CC the invention are used in the study and regulation of cell and tissue
CC development, as components of cell culture media and as diagnostic
CC agents. The zvegfg4 polypeptide can be used in treating full-thickness
CC skin wounds, including venous stasis, ulcers and other chronic, non-
CC healing wounds, in fracture repair, skin grafting, in constructive
CC surgery to promote neovascularisation and increase skin flap survival, to
CC establish vascular networks in transplanted cells and tissues, or in
CC treating female reproductive tract disorders, including acute or chronic
CC placental insufficiency and prolonged bleeding. It can also be used to
CC promote endothelialisation of vascular grafts and stents, in treating
CC acute or chronic lesions of the gastrointestinal tract or treating or
CC repairing liver damage. Zvegfg4 can also be used for treating hepatic
CC chronic passive congestion (CPC) and central haemorrhagic necrosis (CHN).
CC Zvegfg4 proteins, agonists and antagonists can also be used to modulate
CC neurite growth and development and demarcate nervous system structures.
CC It can also be used for treating peripheral neuropathies or
CC neurodegenerative diseases including multiple sclerosis, Alzheimer's
CC disease or Parkinson's disease. The polypeptides, nucleic acids and
CC antibodies can also be used to diagnose or treat disorders associated
CC with cell loss or abnormal cell proliferation (including cancer). The
CC invention is useful in gene therapy. The present sequence is a fusion
CC protein used in the invention.
XX
XX Sequence 302 AA;
SQ
Query Match 100.0%; Score 631; DB 8; Length 302;
Best Local Similarity 100.0%; Pred. No. 8.8e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 VDRLNDADKRYSCPTPNYSVNIREELKLANVVFPRCLLVQRCGNCGGCTVNRSC 60

Db 190 VDRLNDADKRYSCPTPNYSVNIREELKLANVVFPRCLLVQRCGNCGGCTVNRSC 249
Qy 61 CNSGKTWKYKHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
Db 250 CNSGKTWKYKHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 302
RESULT 15
ABU72442
ID ABU72442 standard; protein; 316 AA.
XX
XX AC ABU72442;
XX
XX DT 16-JUN-2003 (first entry)
XX
XX DE ZVEGF4-related fusion protein #2.
XX
XX Growth factor homologue; ZVEGF4; proliferation; differentiation;
KW migration; mesenchymal cell; cell surface semaphorin; neuropilin;
KW neurite growth; cardiovascular development; limb development;
KW cartilage development; T-cell; B-cell; rheumatoid arthritis; cancer;
KW autoimmune disease; inflammation; retinopathy; haemangioma;
KW ischaemic event; neuropathy; acute nerve damage; stroke;
KW central nervous system disease; peripheral nervous system disease.
XX
XX Unidentified.
OS
XX US6495668-B1.
XX
XX PD 17-DEC-2002.
XX
XX PF 03-MAY-2000; 2000US-00564595.
XX
XX PR 03-MAY-1999; 99US-0132250P.
PR 10-NOV-1999; 99US-0164463P.
PR 04-FEB-2000; 2000US-0180169P.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
PI
XX
XX WPI; 2003-352153/33.
XX
XX Isolated growth factor analogue ZVEGF4 proteins for pharmaceutical
PT composition as, e.g. therapeutic agents, diagnostic agents, and research
PT tools and reagents, includes polypeptides from amino acid residues.
XX
XX Claim 14; Col 109-112; 67pp; English.
XX
XX The invention relates to an isolated protein comprising a first
CC polypeptide disulphide-bonded to a second polypeptide. The first and
CC second polypeptides are from 113-138 amino acid residues and comprises
CC 258-370 amino acid residues of human growth factor homologue ZVEGF4. The
CC protein stimulates proliferation, differentiation, or migration of
CC mesenchymal cells and may modulate activities mediated by cell surface
CC semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-
CC semaphorin interactions which may be of use in neurite growth,
CC cardiovascular development, cartilage and limb development, T- and B-cell
CC functions as well as treating rheumatoid arthritis, various forms of
CC cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas,
CC ischaemic events, neuropathies, acute nerve damage, central nervous
CC system diseases and peripheral nervous system diseases including stroke.
CC The isolated protein is also used for a pharmaceutical composition as
CC therapeutic agents, diagnostic agents, and research tools and reagents.
CC It can be used in the study and regulation of cell and tissue
CC development, as components of cell culture media. The proteins can form
CC homomultimers or heteromultimers that act on tissues to control organ
CC development by modulating cell proliferation, migration, differentiation,
CC or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3
CC -23.1. The present sequence represents a ZVEGF4-related fusion protein
CC (claimed but not further defined in the specification)
XX


```
SQ Sequence 316 AA;
Query Match 100.0%; Score 631; DB 6; Length 316;
Best Local Similarity 100.0%; Pred. No. 9.3e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDLRLNDKAKRYSCTPRNYSVNIREELKLANVFPFRCCLLVQRCGNGCGCTVNRST 60
DB 204 VDLRLNDKAKRYSCTPRNYSVNIREELKLANVFPFRCCLLVQRCGNGCGCTVNRST 263
QY 61 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRP 113
DB 264 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRP 316

RESULT 16
ADJ32808
ID ADJ32808 standard; protein; 316 AA.
AC ADJ32808;
XX
XX
XX 15-APR-2004 (first entry)
XX
XX Fusion protein #2 used in the invention.
XX
KW Growth factor homologue; zvegfg4; skin wound; venous stasis; ulcer;
KW fracture repair; skin grafting; neovascularisation;
KW female reproductive tract disorder; bleeding; gastrointestinal tract;
KW liver damage; hepatic chronic passive congestion; CPC;
KW central haemorrhagic necrosis; CHN; neurite growth; neuropathy;
KW neurodegenerative disease; multiple sclerosis; Alzheimer's disease;
KW Parkinson's disease; cell proliferation; cancer; gene therapy.
XX
OS Unidentified.
XX
XX US2004002140-A1.
XX
XX 01-JAN-2004.
XX
XX 06-JUN-2001; 2001US-00876813.
XX
XX 03-MAY-1999; 99US-0132250P.
XX
XX 10-NOV-1999; 99US-0164463P.
XX
XX 04-FEB-2000; 2000US-0180169P.
XX
XX 03-MAY-2000; 2000US-0056459S.
XX
XX (GILB/) GILBERT T.
XX (HART/) HART C E.
XX (SHEP/) SHEPPARD P O.
XX (GILB/) GILBERTSON D G.
XX
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
XX
XX WPI; 2004-070738/07.
XX
XX
XX New zvegfg4 polypeptides and nucleic acids, useful for diagnosing or
XX treating cell loss or abnormal cell proliferation, e.g. cancer, treating
XX full-thickness skin wounds or treating female reproductive tract
XX disorders.
XX
XX Disclosure; SEQ ID NO 55; 73pp; English.
XX
XX
XX The invention relates to growth factor homologue zvegfg4, its
XX corresponding nucleic acid and methods of using them. The sequences of
XX the invention are used in the study and regulation of cell and tissue
XX development, as components of cell culture media and as diagnostic
XX agents. The zvegfg4 polypeptide can be used in treating full-thickness
XX skin wounds, including venous stasis, ulcers and other chronic, non-
XX healing wounds, in fracture repair, skin grafting, in constructive
XX surgery to promote neovascularisation and increase skin flap survival, to
XX establish vascular networks in transplanted cells and tissues, or in
XX treating female reproductive tract disorders, including acute or chronic
XX placental insufficiency and prolonged bleeding. It can also be used to
```

```
CC promote endothelialisation of vascular grafts and stents, in treating
CC acute or chronic lesions of the gastrointestinal tract or treating or
CC repairing liver damage. Zvegfg4 can also be used for treating hepatic
CC chronic passive congestion (CPC) and central haemorrhagic necrosis (CHN).
CC Zvegfg4 proteins, agonists and antagonists can also be used to modulate
CC neurite growth and development and demarcate nervous system structures.
CC It can also be used for treating peripheral neuropathies or
CC neurodegenerative diseases including multiple sclerosis, Alzheimer's
CC disease or Parkinson's disease. The polypeptides, nucleic acids and
CC antibodies can also be used to diagnose or treat disorders associated
CC with cell loss or abnormal cell proliferation (including cancer). The
CC invention is useful in gene therapy. The present sequence is a fusion
CC protein used in the invention.
XX
XX SQ Sequence 316 AA;
Query Match 100.0%; Score 631; DB 8; Length 316;
Best Local Similarity 100.0%; Pred. No. 9.3e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDLRLNDKAKRYSCTPRNYSVNIREELKLANVFPFRCCLLVQRCGNGCGCTVNRST 60
DB 204 VDLRLNDKAKRYSCTPRNYSVNIREELKLANVFPFRCCLLVQRCGNGCGCTVNRST 263
QY 61 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRP 113
DB 264 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRP 316

RESULT 17
ABG75790
ID ABG75790 standard; protein; 317 AA.
XX
XX AC ABG75790;
XX
XX DT 30-APR-2003 (first entry)
XX
XX DE Human growth factor, A.ctg12831-000000.10.0, protein.
XX
XX Human; growth factor; A.ctg12831-000000.10.0;
XX secreted cellular growth factor; cell surface receptor; cellular pathway;
XX signalling pathway; embryonic patterning; cell cycle control; apoptosis;
XX cellular differentiation; cell motility; gene expression; gene therapy;
XX developmental disorder; growth disorder; cardiovascular disorder;
XX neurological disorder; metabolic disorder; cancer; immunological disease;
XX diabetes; osteoporosis; hypercalcaemia; hyperparathyroid; osteopathic;
XX cytostatic; cardiovascular; neuroprotective; immunomodulator.
XX
XX OS Homo sapiens.
XX
XX PN US2002164709-A1.
XX
XX PD 07-NOV-2002.
XX
XX PF 26-FEB-2002; 2002US-00083853.
XX
XX PR 01-MAR-2001; 2001US-0272663P.
XX
XX PA (AFFY-) AFFYMETRIX INC.
XX
XX PI Shigeta RT, Siani-Rose MA;
XX
XX WPI; 2003-247257/24.
XX
XX PT New polynucleotide encoding growth factor, and its encoded protein,
XX useful for diagnosing or treating disorders associated with dysfunction
XX of the growth factors, e.g. diabetes, osteoporosis, hypercalcaemia or
XX hyperparathyroid.
XX
XX PS Claim 7; Fig 1A; 45pp; English.
XX
XX The invention discloses an isolated human growth factor polynucleotide,
XX designated A.ctg12831-000000.10.0, and the polypeptide it encodes.
CC
```

CC Secreted cellular growth factors are molecules which bind to cell surface
CC receptors to regulate a variety of cellular pathways. Growth factors are
CC important in signalling pathways related to embryonic patterning events,
CC cell cycle control, apoptosis, cellular differentiation, cell motility
CC and gene expression. Also disclosed are methods for identifying
CC modulators or receptors of the growth factor and diagnosing a pathogenic
CC condition, or susceptibility to a pathogenic condition, that is
CC associated with a genetic alteration in the growth factor. The growth
CC factor polynucleotide is useful for diagnosing, prognosing or treating
CC (e.g. gene therapy) disorders that are associated with dysfunction of the
CC growth factors, such as developmental and growth disorders,
CC cardiovascular disorders, neurological disorders, metabolic disorders,
CC cancer or immunological diseases. In particular, the polynucleotide is
CC useful for treating or diagnosing e.g. diabetes, osteoporosis,
CC hypercalcaemia or hyperparathyroid. The polynucleotide or polypeptide is
CC also useful in drug screening, particularly for identifying modulators or
CC receptors of growth factors. The sequence presented is the human growth
CC factor, A.ctg12831-000000.10.0, which is disclosed as being encoded by
CC the DNA presented in ABX11387
XX
SQ Sequence 317 AA;

Query Match	100.0%	Score 631;	DB 6;	Length 317;
Best Local Similarity	100.0%;	Pred. No. 9,3e-62;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	VDRLNDDAKRYSGCTPRNYSVNIREELKLANVVFPPRCLLVQRCGNCGGCTVNRSC	60	
Db	205	VDRLNDDAKRYSGCTPRNYSVNIREELKLANVVFPPRCLLVQRCGNCGGCTVNRSC	264	
Qy	61	CNSGKTVKKYHEVLQFPGHKRGRAKTMAVDIQLDHHERCDCICSSRRPR	113	
Db	265	CNSGKTVKKYHEVLQFPGHKRGRAKTMAVDIQLDHHERCDCICSSRRPR	317	

RESULT 18	
AAAY71129	
ID	AAAY71129 standard; peptide; 322 AA.
XX	
XX	AAAY71129;
XX	
XX	08-SEP-2000 (first entry)
DT	
XX	Human Platelet Derived Growth Factor (PDGF)-D partial polypeptide #2.
DE	
XX	Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnery;
XX	VGFG-G: Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
KW	proliferative; activator; proliferation; differentiation; motility;
KW	growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
KW	atherosclerosis; wound; metastasis.
XX	
XX	
OS	Homo sapiens.
XX	
XX	WO200027879-A1.
PN	
XX	
XX	18-MAY-2000
PD	
XX	10-NOV-1999; 99WO-US026462.
XX	
PR	10-NOV-1998; 98US-0107852P.
PR	28-DEC-1998; 98US-0113997P.
PR	26-AUG-1999; 99US-0150604P.
PR	04-OCT-1999; 99US-0157108P.
PR	05-OCT-1999; 99US-0157756P.
XX	
XX	(LUDW-) LUDWIG INST CANCER RES.
PA	(UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX	
PI	Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;
PI	Oestman A, Heidlin C;
XX	
XX	WPI; 2000-376495/32.
DR	N-PSDB; AAD00737.
DR	

XX	Novel polynucleotides encoding a novel growth factor of cells expressing
PT	a platelet-derived growth factor, useful for diagnostic and therapeutic
PT	applications, e.g. concerning cancer.
XX	
PS	Claim 25; Fig 6; 111pp; English.
XX	
CC	The present sequence is an N-terminally truncated polypeptide of human
CC	platelet derived growth factor (PDGF)-D, formally known as Vascular
CC	Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung
CC	lambda2g10 cDNA library. It belongs to the VEGF/PDGF family. It functions
CC	as an activator of proliferation, differentiation, growth and motility of
CC	cells, that express PDGF-D receptor. This sequence is useful for
CC	inhibiting the growth of tumours, that express PDGF-D. Expression of PDGF
CC	-D and its proteolytic cleavage for generating an activated truncated
CC	form is useful for regulating receptor binding specificity of PDGF-D.
CC	PDGF-D antagonist is useful for inhibiting tissue remodelling during the
CC	invasion of tumour cells into normal cells. PDGF-D may be used to treat
CC	wounds, atherosclerosis, metastasis and migration of smooth muscle cells
XX	
SQ	Sequence 322 AA;
	Query Match 100.0%; Score 631; DB 3; Length 322;
	Best Local Similarity 100.0%; Pred. No. 9.5e-62;
	Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 VDLRLNDADKRYSCTPRNVSVNIRELKLNAVVFPRCLLVQRCGNCGCGTWNWSCT 60
Db	210 VDLRLNDADKRYSCTPRNVSVNIRELKLNAVVFPRCLLVQRCGNCGCGTWNWSCT 269
Qy	61 CNSGKTVKKYVHEVLQFPFGHKKRGRAKTWMALVDIQLDHHERCDCICSSRPPR 113
Db	270 CNSGKTVKKYVHEVLQFPFGHKKRGRAKTWMALVDIQLDHHERCDCICSSRPPR 322

Query Match	100.0.0;	Score 631;	DB 3;	Length 322;
Best Local Similarity	100.0.0;	Pred. No. 9.5e-62;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	VDRLNDDAKRYSCTPRNYSVNI	REBLKLANVVFFPRCLLVQRCGNCGGTVNWSCT	60
Db	210	VDRLNDDAKRYSCTPRNYSVNI	REBLKLANVVFFPRCLLVQRCGNCGGTVNWSCT	269
Qy	61	CNSGKTWKYVHEVLQFPFGHI	KRGRAKTWMALVDIQLDHHERCDCI	CSSRPPR 113
Db	270	CNSGKTWKYVHEVLQFPFGHI	KRGRAKTWMALVDIQLDHHERCDCI	CSSRPPR 322

RESULT 19	
ADK68120	
ID	ADK68120 standard; protein; 347 AA.
XX	
AC	ADK68120;
XX	
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Novel NOVX protein #23.
XX	
KW	antiadrenergic; anorectic; cardiac; hypotensive; antiarteriosclerotic;
KW	anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
KW	neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
KW	antiarthritic; antiinflammatory; dermatological; antiasthmatic;
KW	antilipemic; gene therapy; metabolic disorder; diabetes; obesity;
KW	infectious disease; anorexia; cancer; cardiovascular disease;
KW	hypertension; atherosclerosis; neurodegenerative disorder;
KW	Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
KW	osteoarthritis; hematopoietic disorders; inflammatory skin disorder;
KW	asthma; dyslipidemia; neurogenesis; cell differentiation;
KW	cell proliferation; hematopoiesis; wound healing; angiogenesis;
KW	chromosome mapping; pharmacogenomic.
XX	
OS	Homo sapiens.
XX	
XX	
PN	WO2003085124-A2.
XX	
PD	16-OCT-2003.
XX	
XX	01-APR-2003; 2003WO-US009775.
XX	
XX	01-APR-2002; 2002US-0369065P.
PR	03-APR-2002; 2002US-0370279P.
PR	03-APR-2002; 2002US-0370359P.
PR	08-APR-2002; 2002US-0370969P.
PR	12-APR-2002; 2002US-0372019P.
PR	22-APR-2002; 2002US-0374379P.
PR	15-MAY-2002; 2002US-0380973P.

PR 30-MAY-2002; 2002US-0384297P.
PR 30-MAY-2002; 2002US-0384329P.
PR 17-JUN-2002; 2002US-0389729P.
PR 13-AUG-2002; 2002US-0403491P.
PR 15-AUG-2002; 2002US-0403748P.
PR 31-MAR-2003; 2003US-00403142.
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Bento P, Boldog FL, Burgess CE, Casman SJ,
PI Crabtree-Bokor JR, Edinger SR, Ellerman K, Fernandes ER, Gerlach VL;
PI Grosse WM, Gunther E, Gusev VV, Heyes M, Lepley DM, Li L;
PI Macdougall JR, Malyankar UM, Millet I, Patturajan M, Peyman JA;
PI Rastelli L, Rieger DK, Shenoy SG, Shimkets R, Smithson G, Stone DJ;
PI Vernet CAM, Voss E;
XX
XX WPI: 2003-812730/76.
DR N-PSDB; ADK68119.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
XX Claim 1; SEQ ID NO 46; 333pp; English.
XX
XX The invention relates to novel NOVX protein and their encoding DNA's,
CC mature forms of the proteins or sequences that are at least 95% identical
CC to, or having one or more conservative amino acid substitutions in, the
CC proteins. The polypeptides, nucleic acid molecules and antibodies are
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), hematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidemias. The nucleic acids and polypeptides may
CC also be used as targets for the identification of small molecules that
CC modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC corresponds to one of the NOVX proteins of the invention.
XX
XX Sequence 347 AA;
SQ
Query Match 100.0%; Score 631; DB 7; Length 347;
Best Local Similarity 100.0%; Pred. No. 1e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLDRLNDAKYSCTPRNYSVNIRELKLANVVFPPRCLLVQRCGCGGCTVNRST 60
Db 235 VLDRLNDAKYSCTPRNYSVNIRELKLANVVFPPRCLLVQRCGCGGCTVNRST 294
QY 61 CMSGKTVKKYHVLQEPGHIKRGAKTMAVDIQLDHHRCDCICSSRP 113
Db 295 CMSGKTVKKYHVLQEPGHIKRRGRAKTMAVDIQLDHHRCDCICSSRP 347
RESULT 20
ADR49109
ID ADR49109 standard; protein; 347 AA.
XX
XX ADR49109;
XX
XX 04-NOV-2004 (first entry)
XX
XX Human NOV4e protein.

XX
KW NOVX; human; cardiomyopathy; atherosclerosis; hypertension;
KW pulmonary stenosis; obesity; prostate cancer; diabetes; hemophilia;
KW skin disorder; graft versus host disease; AIDS; asthma; lupus;
KW Crohn's disease; inflammatory bowel disease; ulcerative colitis;
KW multiple sclerosis; infectious disease; anorexia; Alzheimer's disease;
KW Parkinson's disease; NOV4e.
XX
OS Homo sapiens.
XX
XX US2004162236-A1.
XX
PD 19-AUG-2004.
XX
XX 31-MAR-2003; 2003US-00403142.
XX
PR 01-APR-2002; 2002US-0369065P.
PR 05-APR-2002; 2002US-0370279P.
PR 05-APR-2002; 2002US-0370359P.
PR 05-APR-2002; 2002US-0370381P.
PR 08-APR-2002; 2002US-0370969P.
PR 12-APR-2002; 2002US-0372019P.
PR 22-APR-2002; 2002US-0374379P.
PR 15-MAY-2002; 2002US-0380973P.
PR 30-MAY-2002; 2002US-0384297P.
PR 30-MAY-2002; 2002US-0384329P.
PR 17-JUN-2002; 2002US-0389729P.
PR 13-AUG-2002; 2002US-0403491P.
PR 15-AUG-2002; 2002US-0403748P.
XX (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLER/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSEV/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
XX
XX Alsobrook J, Bento P, Boldog F, Burgess C, Casman S, Bokor JC;
PI Edinger SR, Ellerman K, Fernandes E, Gerlach V, Grosse W, Gunther E;
PI Gusev V, Heyes M, Lepley D, Li L, Macdougall JR, Malyankar UM;
PI Millet I, Patturajan M, Peyman JA, Rastelli L, Rieger D, Shenoy S;
PI Shimkets R, Smithson G, Stone D, Vernet C, Voss E;
XX
XX WPI: 2004-603580/58.
DR N-PSDB; ADR49108.
XX
XX New isolated polypeptides and nucleic acids, useful for treating or
PT preventing, e.g. cardiomyopathy, atherosclerosis, hypertension, obesity,
PT prostate cancer, diabetes, hemophilia, AIDS, inflammatory bowel disease,
PT or infectious disease.

XX Claim 1; SEQ ID NO 46; 206pp; English.
PS
XX
CC This invention describes novel human NOVX polypeptides and the
CC polynucleotides encoding them. The therapeutic is useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease selected from pathology associated with the polypeptide.
CC Diseases include cardiomyopathy, atherosclerosis, hypertension, pulmonary
CC stenosis, obesity, prostate cancer, diabetes, haemophilia, skin
CC disorders, graft versus host disease, AIDS, asthma, lupus, Crohn's
CC disease, inflammatory bowel disease, ulcerative colitis, multiple
CC sclerosis, infectious disease, anorexia, Alzheimer's disease, or
CC Parkinson's disease. They are also useful in detection assays, chromosome
CC mapping, or tissue typing. This sequence represents the human NOV4e
XX protein.
XX
SQ Sequence 347 AA;
Query Match 100.0%; Score 631; DB 8; Length 347;
Best Local Similarity 100.0%; Pred. No. 1e-61; Mismatches 0; Gaps 0;
Matches 113; Conservative 0; Indels 0;
QY 1 VDLRLNDDAKRYSTPRNYSVNIREEELKLANVVFPRCLLVQRCGNGCGGTVNRSCT 60
Db 235 VDLRLNDDAKRYSTPRNYSVNIREEELKLANVVFPRCLLVQRCGNGCGGTVNRSCT 294
QY 61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHERCDCICSSRP 113
Db 295 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHERCDCICSSRP 347

Search completed: November 10, 2005, 09:31:33
Job time : 56.2774 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:24:47 ; Search time 14.0373 Seconds
(without alignments)
600.925 Million cell updates/sec

Title: US-10-606-055-2_COPY_258_370

Perfect score: 631

Sequence: 1 VDLRLNDKRYSCPRNY.....DIQLDHERCICSSRPPR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/prodata/1/iaa/PCITUS COMB.pep.*

6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	302	4	US-09-564-595D-54
2	631	100.0	316	4	US-09-564-595D-55
3	631	100.0	322	4	US-09-438-046-6
4	631	100.0	370	4	US-09-457-066-37
5	631	100.0	370	4	US-09-540-224-2
6	631	100.0	370	4	US-09-564-595D-2
7	631	100.0	370	4	US-09-706-968-37
8	631	100.0	370	4	US-09-808-972-2
9	631	100.0	370	4	US-09-823-033-5
10	631	100.0	370	4	US-09-438-046-8
11	631	100.0	370	4	US-10-139-583-37
12	631	100.0	370	4	US-10-039-847A-2
13	607	96.2	121	4	US-09-438-046-18
14	607	96.2	200	4	US-09-438-046-4
15	588	93.2	370	4	US-09-540-224-4
16	588	93.2	370	4	US-09-564-595D-53
17	588	93.2	370	4	US-09-808-972-4
18	588	93.2	370	4	US-10-039-847A-4
19	380	60.2	66	4	US-09-438-046-2
20	320	50.7	374	4	US-09-468-647A-118
21	318.5	50.5	132	4	US-09-468-647A-29
22	318.5	50.5	149	4	US-09-468-647A-124
23	318.5	50.5	303	4	US-09-564-595D-57
24	318.5	50.5	317	4	US-09-564-595D-56
25	318.5	50.5	323	4	US-09-468-647A-1
26	318.5	50.5	345	4	US-09-040-220D-2
27	318.5	50.5	345	4	US-09-457-066-2

28	318.5	50.5	345	4	US-09-265-686-2	Sequence 2, Appli
29	318.5	50.5	345	4	US-09-540-224-5	Sequence 5, Appli
30	318.5	50.5	345	4	US-09-564-595D-33	Sequence 33, Appli
31	318.5	50.5	345	4	US-09-706-968-2	Sequence 2, Appli
32	318.5	50.5	345	4	US-09-723-749-2	Sequence 2, Appli
33	318.5	50.5	345	4	US-09-823-033-2	Sequence 2, Appli
34	318.5	50.5	345	4	US-09-468-647A-2	Sequence 2, Appli
35	318.5	50.5	345	4	US-09-468-647A-101	Sequence 101, App
36	318.5	50.5	345	4	US-09-468-647A-103	Sequence 103, App
37	318.5	50.5	345	4	US-09-468-647A-110	Sequence 110, App
38	318.5	50.5	345	4	US-09-468-647A-130	Sequence 130, App
39	318.5	50.5	345	4	US-10-139-583-2	Sequence 2, Appli
40	318.5	50.5	354	4	US-09-468-647A-120	Sequence 120, App
41	318.5	50.5	355	4	US-09-468-647A-122	Sequence 122, App
42	311.5	49.4	345	4	US-09-457-066-43	Sequence 43, Appl
43	311.5	49.4	345	4	US-09-564-595D-35	Sequence 35, Appl
44	311.5	49.4	345	4	US-09-706-968-43	Sequence 43, Appl
45	311.5	49.4	345	4	US-09-823-033-4	Sequence 4, Appli
46	311.5	49.4	345	4	US-10-139-583-43	Sequence 43, Appl
47	308.5	48.9	113	4	US-09-468-647A-99	Sequence 99, Appl
48	292	46.3	227	4	US-09-468-647A-114	Sequence 114, App
49	292	46.3	227	4	US-09-468-647A-116	Sequence 116, App
50	118	18.7	24	4	US-09-540-224-9	Sequence 9, Appli
51	118	18.7	24	4	US-09-564-595D-41	Sequence 41, Appl
52	118	18.7	24	4	US-09-808-972-11	Sequence 11, Appl
53	102	16.2	109	3	US-09-469-186-1	Sequence 1, Appli
54	102	16.2	109	4	US-09-469-185-1	Sequence 1, Appli
55	102	16.2	109	4	US-10-100-037-1	Sequence 1, Appli
56	102	16.2	197	4	US-09-431-888-8	Sequence 8, Appli
57	102	16.2	325	3	US-08-915-795-3	Sequence 3, Appli
58	102	16.2	325	4	US-09-296-275-3	Sequence 3, Appli
59	102	16.2	354	3	US-08-915-795-5	Sequence 5, Appli
60	102	16.2	354	4	US-09-296-275-5	Sequence 5, Appli
61	102	16.2	354	4	US-09-375-248-6	Sequence 6, Appli
62	102	16.2	354	4	US-09-468-647A-109	Sequence 109, App
63	102	16.2	354	4	US-09-169-079-22	Sequence 22, Appl
64	102	16.2	354	4	US-09-214-982-1	Sequence 1, Appli
65	102	16.2	362	4	US-09-949-016-11286	Sequence 11286, A
66	100	15.8	110	4	US-09-847-524-6	Sequence 6, Appli
67	100	15.8	321	3	US-08-915-795-9	Sequence 9, Appli
68	100	15.8	321	4	US-09-847-524-4	Sequence 4, Appli
69	100	15.8	321	4	US-09-296-275-9	Sequence 9, Appli
70	100	15.8	358	3	US-08-915-795-8	Sequence 8, Appli
71	100	15.8	358	4	US-09-847-524-2	Sequence 2, Appli
72	100	15.8	358	4	US-09-296-275-8	Sequence 8, Appli
73	100	15.8	358	4	US-09-438-046-15	Sequence 15, Appl
74	95.5	15.1	102	1	US-08-469-427A-2	Sequence 2, Appli
75	95.5	15.1	102	2	US-08-609-443B-2	Sequence 2, Appli
76	95.5	15.1	102	2	US-08-569-063C-2	Sequence 2, Appli
77	95.5	15.1	102	3	US-08-851-896-2	Sequence 2, Appli
78	95.5	15.1	133	1	US-08-469-427A-9	Sequence 9, Appli
79	95.5	15.1	133	2	US-08-609-443B-9	Sequence 9, Appli
80	95.5	15.1	133	2	US-08-569-063C-9	Sequence 9, Appli
81	95.5	15.1	133	3	US-08-851-896-9	Sequence 9, Appli
82	95.5	15.1	188	1	US-08-469-427A-5	Sequence 5, Appli
83	95.5	15.1	188	2	US-08-609-443B-5	Sequence 5, Appli
84	95.5	15.1	188	3	US-08-569-063C-5	Sequence 5, Appli
85	95.5	15.1	188	3	US-08-851-896-5	Sequence 5, Appli
86	95.5	15.1	207	2	US-08-609-443B-13	Sequence 13, Appl
87	95.5	15.1	207	2	US-08-569-063C-13	Sequence 13, Appl
88	95.5	15.1	207	3	US-08-851-896-13	Sequence 13, Appl
89	94	14.9	195	1	US-08-469-427A-7	Sequence 7, Appli
90	94	14.9	195	2	US-08-609-443B-7	Sequence 7, Appli
91	94	14.9	195	3	US-08-569-063C-7	Sequence 7, Appli
92	94	14.9	195	3	US-08-851-896-7	Sequence 7, Appli
93	93	14.7	228	4	US-09-431-888-7	Sequence 7, Appli
94	93	14.7	350	2	US-08-999-811-4	Sequence 4, Appli
95	93	14.7	350	2	US-08-824-996-2	Sequence 2, Appli
96	93	14.7	350	3	US-09-042-105-4	Sequence 4, Appli
97	93	14.7	350	3	US-08-510-133A-33	Sequence 33, Appl
98	93	14.7	350	3	US-08-585-895-33	Sequence 33, Appl
99	93	14.7	350	4	US-10-084-488-4	Sequence 4, Appli
100	93	14.7	419	2	US-08-999-811-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-09-564-595D-54
; Sequence 54, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-54

Query Match          100.0%; Score 631; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 4.4e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDLRLNDDAKRYCTPRNYSVNIREEKLANVFFPRCLLVQRCGNGCGGTVNRSC 60
Db 190 VDLRLNDDAKRYCTPRNYSVNIREEKLANVFFPRCLLVQRCGNGCGGTVNRSC 249

Qy 61 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113
Db 250 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 302

RESULT 2
US-09-564-595D-55
; Sequence 55, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55
```

```
Query Match          100.0%; Score 631; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDLRLNDDAKRYCTPRNYSVNIREEKLANVFFPRCLLVQRCGNGCGGTVNRSC 60
Db 204 VDLRLNDDAKRYCTPRNYSVNIREEKLANVFFPRCLLVQRCGNGCGGTVNRSC 263

Qy 61 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113
Db 264 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 316

RESULT 3
US-09-438-046-6
; Sequence 6, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-6

Query Match          100.0%; Score 631; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.8e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDLRLNDDAKRYCTPRNYSVNIREEKLANVFFPRCLLVQRCGNGCGGTVNRSC 60
Db 210 VDLRLNDDAKRYCTPRNYSVNIREEKLANVFFPRCLLVQRCGNGCGGTVNRSC 269

Qy 61 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113
Db 270 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 322

RESULT 4
US-09-457-066-37
; Sequence 37, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
```

```
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-37

Query Match      100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYSCPTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
Db 258 VDLRLNDKAKRYSCPTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 317

QY 61 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 318 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 370

RESULT 5
US-09-540-224-2
; Sequence 2, Application US/09540224
; Patent No. 6486543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-2

Query Match      100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYSCPTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
Db 258 VDLRLNDKAKRYSCPTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 317

QY 61 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 318 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 370

RESULT 6
US-09-564-595D-2
; Sequence 2, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D

; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-595D-2

Query Match      100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYSCPTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
Db 258 VDLRLNDKAKRYSCPTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 317

QY 61 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 318 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 370

RESULT 7
US-09-706-968-37
; Sequence 37, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-706-968-37

Query Match      100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYSCPTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
Db 258 VDLRLNDKAKRYSCPTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 317

QY 61 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 318 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 370

RESULT 8
US-09-808-972-2
; Sequence 2, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
```

```
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROBLASTIC
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-972-2

Query Match          100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDADKRYCTPRNYSVNIREEELKLANVFFPRCLLVQRCGNGCGGTNNRSCT 60
DB 258 VDLRLNDADKRYCTPRNYSVNIREEELKLANVFFPRCLLVQRCGNGCGGTNNRSCT 317

QY 61 CNSGKTVKYHEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113
DB 318 CNSGKTVKYHEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 370

RESULT 9
US-09-823-033-5
; Sequence 5, Application US/09823033
; Patent No. 6663870
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-5

Query Match          100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDADKRYCTPRNYSVNIREEELKLANVFFPRCLLVQRCGNGCGGTNNRSCT 60
DB 258 VDLRLNDADKRYCTPRNYSVNIREEELKLANVFFPRCLLVQRCGNGCGGTNNRSCT 317

QY 61 CNSGKTVKYHEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113
DB 318 CNSGKTVKYHEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 370

RESULT 10
US-09-438-046-8
```

```
; Sequence 8, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuzi
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D,
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44633
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-8

Query Match          100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDADKRYCTPRNYSVNIREEELKLANVFFPRCLLVQRCGNGCGGTNNRSCT 60
DB 258 VDLRLNDADKRYCTPRNYSVNIREEELKLANVFFPRCLLVQRCGNGCGGTNNRSCT 317

QY 61 CNSGKTVKYHEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113
DB 318 CNSGKTVKYHEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 370

RESULT 11
US-10-139-583-37
; Sequence 37, Application US/10139583
; Patent No. 6814965
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-583-37
```



```
Query Match          100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDADAKRYSCPTPNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
DB 258 VDLRLNDADAKRYSCPTPNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 317

QY 61 CNSGKTVKKYHEVLQPEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
DB 318 CNSGKTVKKYHEVLQPEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 370

RESULT 12
US-10-039-847A-2
; Sequence 2, Application US/10039847A
; Patent No. 6827938
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; TITLE OF INVENTION: KIDNEY FUNCTION
; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039,847A
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; .TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-847A-2

Query Match          100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDADAKRYSCPTPNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
DB 258 VDLRLNDADAKRYSCPTPNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 317

QY 61 CNSGKTVKKYHEVLQPEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
DB 318 CNSGKTVKKYHEVLQPEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 370

RESULT 13
US-09-438-046-18
; Sequence 18, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D,
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 200
; .TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-4

Query Match          96.2%; Score 607; DB 4; Length 200;
Best Local Similarity 97.3%; Pred. No. 1.8e-63;
Matches 110; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDLRLNDADAKRYSCPTPNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
DB 88 VDLRLNDADAKRYSCPTPNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 147

QY 61 CNSGKTVKKYHEVLQPEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
DB 148 CNSGKTVKKYHEVLQPEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 200
```

```
Query Match          96.2%; Score 607; DB 4; Length 121;
Best Local Similarity 97.3%; Pred. No. 9.7e-64;
Matches 110; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDLRLNDADAKRYSCPTPNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
DB 9 VDLRLNDADAKRYSCPTPNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 68

QY 61 CNSGKTVKKYHEVLQPEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
DB 69 CNSGKTVKKYHEVLQPEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 121

RESULT 14
US-09-438-046-4
; Sequence 4, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D,
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 200
; .TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-4

Query Match          96.2%; Score 607; DB 4; Length 200;
Best Local Similarity 97.3%; Pred. No. 1.8e-63;
Matches 110; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDLRLNDADAKRYSCPTPNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
DB 88 VDLRLNDADAKRYSCPTPNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 147

QY 61 CNSGKTVKKYHEVLQPEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
DB 148 CNSGKTVKKYHEVLQPEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 200
```

```
RESULT 15
US-09-540-224-4
; Sequence 4, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; EARLIER FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-540-224-4

Query Match      93.2%; Score 588; DB 4; Length 370;
Best Local Similarity 90.3%; Pred. No. 6.5e-61;
Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDLRLNDDAKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGGCGCTVNWRSCT 60
Db 258 VDLRLNDVVKRYCTPRNHSVNLREELKLTNAVFFPRCLLVQRCGGCGCTVNWKSCT 317
QY 61 CNSGKTVKKYHEVLQFEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 318 CSSGKTVKKYHEVLKFEFGHFKRGAKKNMALVDIQLDHHERCDCICSSRPPR 370

RESULT 16
US-09-564-595D-53
; Sequence 53, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-564-595D-53

Query Match      93.2%; Score 588; DB 4; Length 370;
Best Local Similarity 90.3%; Pred. No. 6.5e-61;
Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDLRLNDDAKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGGCGCTVNWRSCT 60
Db 258 VDLRLNDVVKRYCTPRNHSVNLREELKLTNAVFFPRCLLVQRCGGCGCTVNWKSCT 317
QY 61 CNSGKTVKKYHEVLQFEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 318 CSSGKTVKKYHEVLKFEFGHFKRGAKKNMALVDIQLDHHERCDCICSSRPPR 370
```

```
RESULT 17
US-09-808-972-4
; Sequence 4, Application US/09908972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROBLASTIC
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-808-972-4

Query Match      93.2%; Score 588; DB 4; Length 370;
Best Local Similarity 90.3%; Pred. No. 6.5e-61;
Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDLRLNDDAKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGGCGCTVNWRSCT 60
Db 258 VDLRLNDVVKRYCTPRNHSVNLREELKLTNAVFFPRCLLVQRCGGCGCTVNWKSCT 317
QY 61 CNSGKTVKKYHEVLQFEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 318 CSSGKTVKKYHEVLKFEFGHFKRGAKKNMALVDIQLDHHERCDCICSSRPPR 370

RESULT 18
US-10-039-847A-4
; Sequence 4, Application US/10039847A
; Patent No. 6827938
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; TITLE OF INVENTION: KIDNEY FUNCTION
; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039,847A
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-039-847A-4

Query Match      93.2%; Score 588; DB 4; Length 370;
Best Local Similarity 90.3%; Pred. No. 6.5e-61;
Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDLRLNDDAKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGGCGCTVNWRSCT 60
```


This Page Blank (uspto)

Result No.	Query %			Description	
	Score	Match	Length	ID	
1	631	100.0	123	16	US-10-403-142-42
2	631	100.0	132	14	US-10-011-364-6
3	631	100.0	132	15	US-10-321-962-6
4	631	100.0	132	16	US-10-403-142-38
5	631	100.0	132	20	US-11-096-308-4
6	631	100.0	152	15	US-10-276-774-2067
7	631	100.0	154	14	US-10-011-364-12
8	631	100.0	154	15	US-10-321-962-12
9	631	100.0	302	11	US-09-876-813-54
10	631	100.0	302	16	US-10-877-623-54
11	631	100.0	316	11	US-09-876-813-55
					Sequence 42, Appl
					Sequence 6, Appl
					Sequence 6, Appl
					Sequence 38, Appl
					Sequence 4, Appl
					Sequence 2067, Ap
					Sequence 12, Appl
					Sequence 12, Appl
					Sequence 54, Appl
					Sequence 55, Appl

85 631 100.0 364 14 US-10-125-926A-186 Sequence 186, App
86 631 100.0 364 14 US-10-125-930A-186 Sequence 186, App
87 631 100.0 364 14 US-10-127-831A-186 Sequence 186, App
88 631 100.0 364 14 US-10-127-837A-186 Sequence 186, App
89 631 100.0 364 14 US-10-127-838B-186 Sequence 186, App
90 631 100.0 364 14 US-10-127-842A-186 Sequence 186, App
91 631 100.0 364 14 US-10-127-843A-186 Sequence 186, App
92 631 100.0 364 14 US-10-127-845A-186 Sequence 186, App
93 631 100.0 364 14 US-10-127-846A-186 Sequence 186, App
94 631 100.0 364 14 US-10-127-848A-186 Sequence 186, App
95 631 100.0 364 14 US-10-127-849A-186 Sequence 186, App
96 631 100.0 364 14 US-10-127-850A-186 Sequence 186, App
97 631 100.0 364 14 US-10-127-851A-186 Sequence 186, App
98 631 100.0 364 14 US-10-128-684A-186 Sequence 186, App
99 631 100.0 364 14 US-10-128-686A-186 Sequence 186, App
100 631 100.0 364 14 US-10-128-690A-186 Sequence 186, App

ALIGNMENTS

RESULT 1
US-10-403-142-42
; Sequence 42, Application US/10403142
; Publication No. US20040162236A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-573A
; CURRENT APPLICATION NUMBER: US/10/403,142
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 08/969106
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 09/544511
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/369065
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/604286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/651200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 09/662783
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/688598
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/894159
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/918779
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 09/964956
; PRIOR FILING DATE: 2001-09-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 42
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-142-42

Query Match 100.0%; Score 631; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.8e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VDLRLNDKRYCTPRNYSVNIREELKLANVVFPRCLLVQRCGNCGGTVNRSC 60
Db 11 VDLRLNDKRYCTPRNYSVNIREELKLANVVFPRCLLVQRCGNCGGTVNRSC 70
Oy 61 CNSGKTVKHYEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPP 113
Db 71 CNSGKTVKHYEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPP 123

RESULT 2
US-10-011-364-6
; Sequence 6, Application US/10011364
; Publication No. US20030153495A1
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henry
; APPLICANT: Jeffers, Michael
; APPLICANT: Shimkets, Richard
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Boldog, Ferenc
; APPLICANT: Yang, Meijia
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Rittman, B.
; APPLICANT: Shimkets, Juliette
; APPLICANT: Larochele, William
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease Using Growth
; FILE REFERENCE: 15966-557A IBD CIP
; CURRENT APPLICATION NUMBER: US/10/011,364
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/246,206
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 09/992,840
; PRIOR FILING DATE: 2001-11-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-364-6

Query Match 100.0%; Score 631; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 3e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VDLRLNDKRYCTPRNYSVNIREELKLANVVFPRCLLVQRCGNCGGTVNRSC 60
Db 20 VDLRLNDKRYCTPRNYSVNIREELKLANVVFPRCLLVQRCGNCGGTVNRSC 79
Oy 61 CNSGKTVKHYEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPP 113
Db 80 CNSGKTVKHYEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPP 132

RESULT 3
US-10-321-962-6
; Sequence 6, Application US/10321962
; Publication No. US20040006015A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Fernandes, Elma
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Larochele, William J.
; APPLICANT: Lichenstein, Henry S.
; APPLICANT: Peterson, Jeffrey
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Rittman, Beth
; APPLICANT: Shimkets, Juliette
; APPLICANT: Yang, Meijia
; APPLICANT: Curagen Corporation
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease
; FILE REFERENCE: 15966-557A IBD CIP2
; CURRENT APPLICATION NUMBER: US/10/321,962
; CURRENT FILING DATE: 2002-12-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 6
; LENGTH: 132

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-962-6

Query Match      100.0%; Score 631; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 3e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKYSCPTPRNYSVNIREEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 60
    |||||
Db 20 VDLRLNDKAKYSCPTPRNYSVNIREEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 79
    |||||

QY 61 CNSGKTVKKYHEVLPFGHKKRGRKTMALVDIQLDHHRCDCICSSRRPPR 113
    |||||
Db 80 CNSGKTVKKYHEVLPFGHKKRGRKTMALVDIQLDHHRCDCICSSRRPPR 132
    |||||

RESULT 4
US-10-403-142-38
; Sequence 38, Application US/10403142
; Publication No. US20040162236A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-573A
; CURRENT APPLICATION NUMBER: US/10/403,142
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 08/969106
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 09/544511
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/369065
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/604286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/651200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 09/662783
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/688598
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/894159
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/918779
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 09/964956
; PRIOR FILING DATE: 2001-09-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 38
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-142-38

Query Match      100.0%; Score 631; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 3e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKYSCPTPRNYSVNIREEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 60
    |||||
Db 20 VDLRLNDKAKYSCPTPRNYSVNIREEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 79
    |||||

QY 61 CNSGKTVKKYHEVLPFGHKKRGRKTMALVDIQLDHHRCDCICSSRRPPR 113
    |||||
Db 80 CNSGKTVKKYHEVLPFGHKKRGRKTMALVDIQLDHHRCDCICSSRRPPR 132
    |||||

RESULT 5
US-11-096-308-4
; Sequence 4, Application US/11096308
; Publication No. US20050171020A1
; GENERAL INFORMATION:
; APPLICANT: Shinketsu, Richard A.
; APPLICANT: Herrmann, John
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Growth Factor Polypeptides and Nucleic Acids Encoding
; TITLE OF INVENTION: Same
; FILE REFERENCE: 15966-577 CON (Cura-77 CON)
; CURRENT APPLICATION NUMBER: US/11/096,308
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: USSN 09/662,783
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: USSN 60/158,083
; PRIOR FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: USSN 60/186,707
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: USSN 60/188,250
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: USSN 60/159,231
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: USSN 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: USSN 60/223,879
; PRIOR FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-308-4

Query Match      100.0%; Score 631; DB 20; Length 132;
Best Local Similarity 100.0%; Pred. No. 3e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKYSCPTPRNYSVNIREEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 60
    |||||
Db 20 VDLRLNDKAKYSCPTPRNYSVNIREEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 79
    |||||

QY 61 CNSGKTVKKYHEVLPFGHKKRGRKTMALVDIQLDHHRCDCICSSRRPPR 113
    |||||
Db 80 CNSGKTVKKYHEVLPFGHKKRGRKTMALVDIQLDHHRCDCICSSRRPPR 132
    |||||

RESULT 6
US-10-276-774-2067
; Sequence 2067, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y. Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2067
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2067

Query Match      100.0%; Score 631; DB 15; Length 152;
Best Local Similarity 100.0%; Pred. No. 3.5e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKYSCPTPRNYSVNIREEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 60
```

```
Db 40 VDLRLNDADAKRYCTPRNYSVNIREELKLANVVFPRCLLVQRCGGCGGTNNRSCT 99
Qy 61 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRRPR 113
Db 100 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRRPR 152
```

RESULT 7

```
US-10-011-364-12
; Sequence 12, Application US/10011364
; Publication No. US20030153495A1
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henry
; APPLICANT: Jeffers, Michael
; APPLICANT: Shinkets, Richard
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Boldog, Ferenc
; APPLICANT: Yang, Meijia
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Rittman, B.
; APPLICANT: Shinkets, Juliette
; APPLICANT: LaRochele, William
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease Using Growth
; TITLE OF INVENTION: Factors
; FILE REFERENCE: 15966-557A IBD CIP
; CURRENT APPLICATION NUMBER: US/10/011,364
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/246,206
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 09/992,840
; PRIOR FILING DATE: 2001-11-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 12
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-364-12
```

```
Query Match 100.0%; Score 631; DB 14; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDLRLNDADAKRYCTPRNYSVNIREELKLANVVFPRCLLVQRCGGCGGTNNRSCT 60
Db 42 VDLRLNDADAKRYCTPRNYSVNIREELKLANVVFPRCLLVQRCGGCGGTNNRSCT 101
Qy 61 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRRPR 113
Db 102 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRRPR 154
```

RESULT 8

```
US-10-321-962-12
; Sequence 12, Application US/10321962
; Publication No. US20040006015A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Fernandes, Elma
; APPLICANT: Jeffers, Michael E.
; APPLICANT: LaRochele, William J.
; APPLICANT: Lichenstein, Henry S.
; APPLICANT: Peterson, Jeffrey
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Rittman, Beth
; APPLICANT: Shinkets, Juliette
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Yang, Meijia
; APPLICANT: CuraGen Corporation
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease
```

```
; TITLE OF INVENTION: Using Growth Factors
; FILE REFERENCE: 15966-557A IBD CIP2
; CURRENT APPLICATION NUMBER: US/10/321,962
; CURRENT FILING DATE: 2002-12-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 12
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-962-12
```

```
Query Match 100.0%; Score 631; DB 15; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDLRLNDADAKRYCTPRNYSVNIREELKLANVVFPRCLLVQRCGGCGGTNNRSCT 60
Db 42 VDLRLNDADAKRYCTPRNYSVNIREELKLANVVFPRCLLVQRCGGCGGTNNRSCT 101
Qy 61 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRRPR 113
Db 102 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRRPR 154
```

RESULT 9

```
US-09-876-813-54
; Sequence 54, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-876-813-54
```

```
Query Match 100.0%; Score 631; DB 11; Length 302;
Best Local Similarity 100.0%; Pred. No. 7.5e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDLRLNDADAKRYCTPRNYSVNIREELKLANVVFPRCLLVQRCGGCGGTNNRSCT 60
Db 190 VDLRLNDADAKRYCTPRNYSVNIREELKLANVVFPRCLLVQRCGGCGGTNNRSCT 249
Qy 61 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRRPR 113
Db 250 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRRPR 302
```

RESULT 10

```
US-10-877-623-54
; Sequence 54, Application US/10877623
; Publication No. US20040242850A1
; GENERAL INFORMATION:
```



```

; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/10/877,623
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US/09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US/60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US/60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
; US-10-877-623-54

Query Match          100.0%; Score 631; DB 16; Length 302;
Best Local Similarity 100.0%; Pred. No. 7.5e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAYSCSTPRNYSVNIREEELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
DB 190 VDLRLNDKAYSCSTPRNYSVNIREEELKLANVVFPRCLLVORCGNCGCGTVNWRSC 249

QY 61 CNSGKTVKKYHEVLOPEPGHKKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
DB 250 CNSGKTVKKYHEVLOPEPGHKKRRGAKTMALVDIQLDHHERCDCICSSRPPR 302

RESULT 11
US-09-876-813-55
; Sequence 55, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US/09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US/60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US/60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
; US-09-876-813-55

Query Match          100.0%; Score 631; DB 11; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.9e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-876-813-55
; Sequence 55, Application US/10877623
; Publication No. US20040242850A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/10/877,623
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US/09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US/60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US/60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
; US-10-877-623-55

Query Match          100.0%; Score 631; DB 16; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.9e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAYSCSTPRNYSVNIREEELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
DB 204 VDLRLNDKAYSCSTPRNYSVNIREEELKLANVVFPRCLLVORCGNCGCGTVNWRSC 263

QY 61 CNSGKTVKKYHEVLOPEPGHKKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
DB 264 CNSGKTVKKYHEVLOPEPGHKKRRGAKTMALVDIQLDHHERCDCICSSRPPR 316

RESULT 12
US-10-877-623-55
; Sequence 55, Application US/10877623
; Publication No. US20040242850A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/10/877,623
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US/09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US/60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US/60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
; US-10-877-623-55

Query Match          100.0%; Score 631; DB 16; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.9e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAYSCSTPRNYSVNIREEELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
DB 204 VDLRLNDKAYSCSTPRNYSVNIREEELKLANVVFPRCLLVORCGNCGCGTVNWRSC 263

QY 61 CNSGKTVKKYHEVLOPEPGHKKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
DB 264 CNSGKTVKKYHEVLOPEPGHKKRRGAKTMALVDIQLDHHERCDCICSSRPPR 316

RESULT 13
US-10-083-853-2
; Sequence 2, Application US/10083853
; Publication No. US20020164709A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc
; APPLICANT: Shigeta, Ron T
; APPLICANT: Siani-Rose, Michael A
; TITLE OF INVENTION: Nucleic Acid Encoding Growth Factor Protein
; FILE REFERENCE: 3385.1
; CURRENT APPLICATION NUMBER: US/10/083,853
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: USSN 60/272,663
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 317
```

```
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-083-853-2

Query Match      100.0%; Score 631; DB 13; Length 317;
Best Local Similarity 100.0%; Pred. No. 7.9e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDLRLNDADKRYCTPNYSVNIREELKLANVVFPRCLLVQRCGCGCTVNRST 60
Db 205 VDLRLNDADKRYCTPNYSVNIREELKLANVVFPRCLLVQRCGCGCTVNRST 264
Qy 61 CNSGKTVKYHEVLQFEGHFKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
Db 265 CNSGKTVKYHEVLQFEGHFKRRGRKTMALVDIQLDHHRCDCICSSRPPR 317

RESULT 14
US-10-086-623-6
; Sequence 6, Application US/10086623
; Publication No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THEREFOR
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-623-6

Query Match      100.0%; Score 631; DB 13; Length 322;
Best Local Similarity 100.0%; Pred. No. 8e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDLRLNDADKRYCTPNYSVNIREELKLANVVFPRCLLVQRCGCGCTVNRST 60
Db 210 VDLRLNDADKRYCTPNYSVNIREELKLANVVFPRCLLVQRCGCGCTVNRST 269
Qy 61 CNSGKTVKYHEVLQFEGHFKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
Db 270 CNSGKTVKYHEVLQFEGHFKRRGRKTMALVDIQLDHHRCDCICSSRPPR 322

RESULT 15
US-10-260-539-6
; Sequence 6, Application US/10260539
; Publication No. US20030073637A1
```

```
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THEREFOR
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/260,539
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-260-539-6

Query Match      100.0%; Score 631; DB 14; Length 322;
Best Local Similarity 100.0%; Pred. No. 8e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDLRLNDADKRYCTPNYSVNIREELKLANVVFPRCLLVQRCGCGCTVNRST 60
Db 210 VDLRLNDADKRYCTPNYSVNIREELKLANVVFPRCLLVQRCGCGCTVNRST 269
Qy 61 CNSGKTVKYHEVLQFEGHFKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
Db 270 CNSGKTVKYHEVLQFEGHFKRRGRKTMALVDIQLDHHRCDCICSSRPPR 322

RESULT 16
US-10-794-392-6
; Sequence 6, Application US/10794392
; Publication No. US20050209136A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THEREFOR
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/794,392
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/10/260,539
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
```

```
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent version 3.1
; SEQ ID NO 6
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-392-6

Query Match      100.0%; Score 631; DB 18; Length 322;
Best Local Similarity 100.0%; Pred. No. 8e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKYSCPTPRNYSNIREELKLANVVFPRCLLVORCGNCGCGTVNWSCT 60
Db 210 VDLRLNDKAKYSCPTPRNYSNIREELKLANVVFPRCLLVORCGNCGCGTVNWSCT 269

QY 61 CMSGKTVKKYHEVLPQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 270 CMSGKTVKKYHEVLPQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 322

RESULT 17
US-10-403-142-46
; Sequence 46, Application US/10403142
; Publication No. US20040162236A1
; GENERAL INFORMATION:
; APPLICANT: Alsebrook et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-573A
; CURRENT APPLICATION NUMBER: US/10/403,142
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 08/969106
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 09/544511
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/369065
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/604286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/651200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 09/662783
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/688598
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/894159
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/918779
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 09/964956
; PRIOR FILING DATE: 2001-09-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 46
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-142-46

Query Match      100.0%; Score 631; DB 16; Length 347;
Best Local Similarity 100.0%; Pred. No. 8.7e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKYSCPTPRNYSNIREELKLANVVFPRCLLVORCGNCGCGTVNWSCT 60
Db 235 VDLRLNDKAKYSCPTPRNYSNIREELKLANVVFPRCLLVORCGNCGCGTVNWSCT 294

QY 61 CMSGKTVKKYHEVLPQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 295 CMSGKTVKKYHEVLPQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 347

RESULT 18
US-10-028-072-186
; Sequence 186, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062814
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
```

; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063127
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063561
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063704
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063733
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063735
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063738
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064248
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/064809
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065846
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066453
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069212
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069278
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069334
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069694
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 60/072320
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 60/073612
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074092
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081695
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15

; PRIOR APPLICATION NUMBER: 60/081818
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086414
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086430
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 19/98-06-11
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match 100.0%; Score 631; DB 14; Length 364;
Best Local Similarity 100.0%; Pred. No. 9.2e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYCTPRNYSNIREELKLANVFFPRCLLVQRCGGCGCTVNRSC 60
DB 252 VDLRLNDKAKRYCTPRNYSNIREELKLANVFFPRCLLVQRCGGCGCTVNRSC 311
QY 61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHRCDCICSSRPP 113
DB 312 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHRCDCICSSRPP 364

RESULT 19

US-10-140-808-186
; Sequence 186, Application US/10140808
; Publication No. US20030017563A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 186
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-186

Query Match 100.0%; Score 631; DB 14; Length 364;
Best Local Similarity 100.0%; Pred. No. 9.2e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYCTPRNYSNIREELKLANVFFPRCLLVQRCGGCGCTVNRSC 60
DB 252 VDLRLNDKAKRYCTPRNYSNIREELKLANVFFPRCLLVQRCGGCGCTVNRSC 311
QY 61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHRCDCICSSRPP 113
DB 312 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHRCDCICSSRPP 364

RESULT 20

US-10-121-049-186
; Sequence 186, Application US/10121049
; Publication No. US2003002239A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 186
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-186

Query Match 100.0%; Score 631; DB 14; Length 364;
Best Local Similarity 100.0%; Pred. No. 9.2e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYCTPRNYSNIREELKLANVFFPRCLLVQRCGGCGCTVNRSC 60
DB 252 VDLRLNDKAKRYCTPRNYSNIREELKLANVFFPRCLLVQRCGGCGCTVNRSC 311
QY 61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHRCDCICSSRPP 113
DB 312 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHRCDCICSSRPP 364

Search completed: November 10, 2005, 09:41:03
Job time : 52.7039 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:24:01 ; Search time 11.9317 Seconds
(without alignments)
911.229 Million cell updates/sec

Title: US-10-606-055-2_COPY_258_370
Perfect score: 631
Sequence: 1 VLDRLNDKAKRYSCPRNY.....DIQLDHERCICSSRPPR 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 79: *
1: Piri: *
2: Piri2: *
3: Piri3: *
4: Piri4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	370	2 JC7591	spinal cord-derive
2	588	93.2	370	2 JC7998	platelet-derived g
3	585	92.7	370	2 JC7592	spinal cord-derive
4	100.5	15.9	148	2 D49530	16K vascular endot
5	95.5	15.1	188	2 JC4680	vascular endotheli
6	95.5	15.1	207	2 JC4679	vascular endotheli
7	94	14.9	166	2 JN0248	platelet-derived g
8	94	14.9	198	2 JS0735	platelet-derived g
9	93	14.7	419	2 S69207	vascular endotheli
10	89	14.1	196	2 A37359	platelet-derived g
11	89	14.1	196	2 A48851	platelet-derived g
12	89	14.1	196	2 B28964	platelet-derived g
13	89	14.1	197	2 S25096	platelet-derived g
14	89	14.1	211	1 PFHUG1	platelet-derived g
15	84.5	13.4	133	2 B49530	vascular endotheli
16	83.5	13.2	80	2 T03404	metallothionein-li
17	83	13.2	200	2 IS1551	platelet-derived g
18	83	13.2	215	2 S08220	platelet-derived g
19	83	13.2	226	2 IS1550	platelet-derived g
20	79	12.5	241	1 PFMSG8	platelet-derived g
21	78.5	12.4	80	2 T02063	metallothionein-li
22	78	12.4	225	2 S25097	platelet-derived g
23	78	12.4	297	2 G71265	hypothetical prote
24	77	12.2	77	2 S26336	metallothionein -
25	77	12.2	120	2 A33787	ovine vascular end
26	77	12.2	146	2 S57956	vascular endotheli
27	77	12.2	190	2 B40080	vascular endotheli
28	77	12.2	245	1 TVCTSS	platelet-derived g
29	76	12.0	241	1 PFHUG2	platelet-derived g

metallothionein-li
metallothionein, t
metallothionein -
metallothionein ty
metallothionein-li
placental growth f
metallothionein-li
metallothionein-li
metallothionein -
metallothionein -
epidermal growth f
epidermal growth f
epidermal growth f
hypothetical prote
hypothetical prote
hypothetical prote
metallothionein-li
glioma-derived vas
vascular endotheli
metallothionein -
placental growth f
hypothetical prote
hypothetical prote
hypothetical prote
metallothionein-li
metallothionein-li
metallothionein 2a
vascular endotheli
vascular endotheli
PDGF-related trans
PDGF-related trans
hypothetical prote
alpha-actinin - Ca
hypothetical prote
metallothionein-li
vascular endotheli
metallothionein -
glycine-rich prote
metallothionein ty
metallothionein-li
metallothionein-li
ribokinase - Metha
hypothetical prote
hypothetical prote
probable polynucle
S-receptor kinase
metallothionein 20
hypothetical prote
vascular endotheli
metallothionein 20
metallothionein 2b
metallothionein-li
hypothetical prote
integrin beta-3 ch
F13B4.3 protein -
fibillin-2 precur
metallothionein-li
gonadotropin II be
PDGF-related trans
hypothetical prote
L-ascorbate oxidas
hypothetical prote
laminin beta-1 cha
mucin 2 precursor,
metallothionein-li
gonadotropin beta
gonadotropin II be
hypothetical prote
integrin beta-3 ch
hypothetical prote
DnI7 protein - yea
60 kDa outer membr
Mutator-like trans
Mutatable ATPase (E
metallothionein 20

See Deleted 11

ALIGNMENTS

```
RESULT 1
JC7591
spinal cord-derived growth factor-B precursor - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7591
R:Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/
A:Reference number: JC7591; MUID:21092670; PMID:11162582
A:Accession: JC7591
A:Molecule type: DNA
A:Residues: 1-370 <HAM>
A:CROSS-references: UNIPROT:Q9BWV5; UNIPROT:Q9GZP0; DDBJ:AB033832
C:Genetics:
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth
F:294-308/Region: conserved motif #status predicted
Query Match 100.0%; Score 631; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 2.7e-57;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDLRLNDADKRYSCPTPNYSVNIREELKLANVFFPRCLLVQRCGCGGVNWSCT 60
DB 258 VDLRLNDADKRYSCPTPNYSVNIREELKLANVFFPRCLLVQRCGCGGVNWSCT 317
QY 61 CNSGKTWKYHEVLQFEGHKKRGRKTMALVDIQLDHHERCDCICSSRPPR 113
DB 318 CNSGKTWKYHEVLQFEGHKKRGRKTMALVDIQLDHHERCDCICSSRPPR 370
RESULT 2
JC7998
platelet-derived growth factor-D - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003
C:Accession: JC7998
R:Zhao, Y.; Hoyle, G.W.; Zhang, J.; Morris, G.; Lasky, J.A.
Biochem. Biophys. Res. Commun. 308, 126-132, 2003
A:Title: A novel murine PDGF-D splicing variant results in significant differences in pe
A:Reference number: JC7998; PMID:12890490
A:Accession: JC7998
A:Molecule type: mRNA
A:Residues: 1-370 <ZHU>
C:Comment: This protein is a potent mesenchymal cell mitogen and chemoattractant involve
C:Genetics:
A:Gene: pdgf-D
A:Introns: 42/2; 110/1; 170/2; 191/2; 258/2; 330/1; 334/2
C:Keywords: fibrosis; PDGF-D
Query Match 93.2%; Score 588; DB 2; Length 370;
Best Local Similarity 90.3%; Pred. No. 7.2e-53;
Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 VDLRLNDADKRYSCPTPNYSVNIREELKLANVFFPRCLLVQRCGCGGVNWSCT 60
DB 258 VDLRLNDADKRYSCPTPNYSVNIREELKLANVFFPRCLLVQRCGCGGVNWSCT 317
QY 61 CNSGKTWKYHEVLQFEGHKKRGRKTMALVDIQLDHHERCDCICSSRPPR 113
DB 318 CNSGKTWKYHEVLQFEGHKKRGRKTMALVDIQLDHHERCDCICSSRPPR 370
RESULT 3
JC7592
spinal cord-derived growth factor-B precursor - rat
```

```
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7592
R:Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/
A:Reference number: JC7591; MUID:21092670; PMID:11162582
A:Contents: Fetal brain
A:Accession: JC7592
A:Molecule type: mRNA
A:Residues: 1-370 <HAM>
A:CROSS-references: UNIPROT:Q9EQTL; DDBJ:AB052170
C:Genetics:
A:Gene: scdgf-B
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth
F:294-308/Region: conserved motif #status predicted
Query Match 92.7%; Score 585; DB 2; Length 370;
Best Local Similarity 89.4%; Pred. No. 1.5e-52;
Matches 101; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 1 VDLRLNDADKRYSCPTPNYSVNIREELKLANVFFPRCLLVQRCGCGGVNWSCT 60
DB 258 VDLRLNDADKRYSCPTPNYSVNIREELKLANVFFPRCLLVQRCGCGGVNWSCT 317
QY 61 CNSGKTWKYHEVLQFEGHKKRGRKTMALVDIQLDHHERCDCICSSRPPR 113
DB 318 CNSGKTWKYHEVLQFEGHKKRGRKTMALVDIQLDHHERCDCICSSRPPR 370
RESULT 4
D49530
16K vascular endothelial growth factor homolog A2R - Orf virus
C:Species: Orf virus
C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: D49530
R:Lyttle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
J. Virol. 68, 84-92, 1994
A:Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus orf
A:Reference number: A49530; MUID:94076465; PMID:8254780
A:Contents: NZ7
A:Accession: D49530
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <LYT>
A:CROSS-references: UNIPROT:P52585; GB:S67522; NID:g456900; PIDN:AAB29223.1; PID:g456902
A:Note: sequence extracted from NCBI backbone (NCBIN:141422, NCBI:P:141426)
Query Match 15.9%; Score 100.5; DB 2; Length 148;
Best Local Similarity 25.6%; Pred. No. 0.0041;
Matches 32; Conservative 13; Mismatches 31; Indels 49; Gaps 5;
QY 15 CTPEYNSVNIREE-LKLANVVFPRCLLVQRCGCG- - - - -CGTVNWSCT- - - - - 60
DB 46 CKPRDTVVYLGEEYPESTNLYQNPRTVTKRSCCGNGDGOICTAVETRTTVTVSTGV 105
QY 61 - - - - -CNSGKTWKYHEVLQFEGHKKRGRKTMALVDIQLDHHERCDCI- - - - -CS 108
DB 106 SSSSGTNSGVSTN- - - - -LQRI SVTEHTKDCICIGRTTTTPTT 142
QY 109 SRPPR 113
DB 143 TREPR 147
RESULT 5
JC4680
vascular endothelial growth factor-related factor 167 precursor - mouse
N:Alternate names: VRF 167 protein
C:Species: Mus musculus (house mouse)
```


C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: JC4680
R:Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.; Nordenskjoeld, M.; Weber, G.; Biochem. Biophys. Res. Commun. 220, 922-928, 1996
A:Title: Characterization of the murine VEGF-related factor gene.
A:Reference number: JC4679; MUID:96183052; PMID:8607868
A:Accession: JC4680
A:Molecule type: mRNA
A:Residues: 1-188 <TOW>
A:Cross-references: UNIPROT:P49766; GB:U43837; NID:G131435; PIDN:AA52553.1; PID:G13143
C:Comment: This factor is a mitogen, that is selective for endothelial cells, and belongs to the VEGF family of endothelial growth factors.
C:Genetics:
A:Gene: vrf
A:Map position: 19
A:Introns: 137/2
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-188/Product: vascular endothelial growth factor-related factor #status predicted <M>

Query Match 15.1%; Score 95.5; DB 2; Length 188;
Best Local Similarity 27.9%; Pred. No. 0.017;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

QY 12 RYSCTPRNYSVNIREFLKLNVV--FFPRCLLVQRCGCGCTVNWRSCTNSGKTVKK 69
Db 44 RATCQPREVVPLSMEL-MGNVVKQLVPSCTVQRCG---GCCPDDGLECVPTGQHQVRM 99
QY 70 YHEVLQFEPGHIKRRGRATKTMALVDIQLDHERCDICSSRPP 113
Db 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPKK 128

RESULT 6
JC4679
vascular endothelial growth factor-related factor 186 precursor - mouse
N:Alternate names: VRF 186 protein, VEGF 186
C:Species: Mus musculus (house mouse)
C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: JC4679
R:Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.; Nordenskjoeld, M.; Weber, G.; Biochem. Biophys. Res. Commun. 220, 922-928, 1996
A:Title: Characterization of the murine VEGF-related factor gene.
A:Reference number: JC4679; MUID:96183052; PMID:8607868
A:Accession: JC4679
A:Molecule type: mRNA
A:Residues: 1-207 <TOW>
A:Cross-references: UNIPROT:P49766; GB:U43836; NID:G1703480; PIDN:AA52932.1; PID:G13143
C:Comment: This factor is a mitogen, that is selective for endothelial cells, and belongs to the VEGF family of endothelial growth factors.
C:Genetics:
A:Gene: vrf
A:Map position: 19
C:Keywords: growth factor
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-207/Product: vascular endothelial growth factor related factor #status predicted <M>

Query Match 15.1%; Score 95.5; DB 2; Length 207;
Best Local Similarity 27.9%; Pred. No. 0.018;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

QY 12 RYSCTPRNYSVNIREFLKLNVV--FFPRCLLVQRCGCGCTVNWRSCTNSGKTVKK 69
Db 44 RATCQPREVVPLSMEL-MGNVVKQLVPSCTVQRCG---GCCPDDGLECVPTGQHQVRM 99
QY 70 YHEVLQFEPGHIKRRGRATKTMALVDIQLDHERCDICSSRPP 113
Db 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPKK 128

RESULT 7
JN0248
platelet-derived growth factor chain A3 precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 27-Jun-1994
C:Accession: JN0248
R:Nakahara, K.; Nishimura, H.; Kuro-o, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazaki, Biochem. Biophys. Res. Commun. 184, 811-818, 1992
A:Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vascular endothelial growth factor gene.
A:Reference number: JN0248; MUID:92246970; PMID:1575749
A:Accession: JN0248
A:Molecule type: mRNA
A:Residues: 1-166 <NAK>
A:Cross-references: UNIPROT:P34007
C:Superfamily: platelet-derived growth factor
F:1-22/Domain: propeptide (fragment) #status predicted <PRO>
F:23-166/Product: platelet-derived growth factor A3 chain #status predicted <MAT>

Query Match 14.9%; Score 94; DB 2; Length 166;
Best Local Similarity 28.0%; Pred. No. 0.021;
Matches 23; Conservative 17; Mismatches 32; Indels 10; Gaps 3;

QY 31 ANNVFPRCLLVQRCGCGCTVNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRATM 90
Db 50 ANFLIWPPECVEVKRTGCC-----NTSSVKCQPSRVHHRSVKVAKE--YVRKKPKLKE- 101
QY 91 ALVDIQLDHERCDICSSRPP 112
Db 102 --VQVRLBEHLCECAASSAGP 121

RESULT 8
JS0735
platelet-derived growth factor chain A1 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C:Accession: JS0735
R:Nakahara, K.; Nishimura, H.; Kuro-o, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazaki, Biochem. Biophys. Res. Commun. 184, 811-818, 1992
A:Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vascular endothelial growth factor gene.
A:Reference number: JN0248; MUID:92246970; PMID:1575749
A:Accession: JS0735
A:Molecule type: mRNA
A:Residues: 1-198 <NAK>
A:Cross-references: UNIPROT:P34007
A:Note: this protein corresponds to the endothelial type of human A chain
C:Superfamily: platelet-derived growth factor
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-89/Domain: propeptide #status predicted <PRO>
F:90-198/Product: platelet-derived growth factor A1 chain #status predicted <MAT>

Query Match 14.9%; Score 94; DB 2; Length 198;
Best Local Similarity 28.0%; Pred. No. 0.025;
Matches 23; Conservative 17; Mismatches 32; Indels 10; Gaps 3;

QY 31 ANNVFPRCLLVQRCGCGCTVNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRATM 90
Db 117 ANFLIWPPECVEVKRTGCC-----NTSSVKCQPSRVHHRSVKVAKE--YVRKKPKLKE- 168
QY 91 ALVDIQLDHERCDICSSRPP 112
Db 169 --VQVRLBEHLCECAASSAGP 188

RESULT 9
S69207
vascular endothelial growth factor C precursor - human
N:Alternate names: FLT4 ligand DHM
C:Species: Homo sapiens (man)
C>Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: S69207; S61795; S71443; S69208; G02859
R:Joukov, V.; Pajusola, K.; Kaipainen, A.; Chillov, D.; Lahinen, I.; Kukk, E.; Saksela, EMBO J. 15, 1751, 1996
A:Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand for VEGFR-2.
A:Reference number: S69207; MUID:96203094; PMID:8612600
A:Accession: S69207
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA

A;Residues: 1-419 <JOU>
A;Cross-references: UNIPROT:P49767; EMBL:X94216; NID:gl1177488; PIDN:CAA63907.1; PID:e221
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A;Note: only a part of the translation is shown
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kuk, E.; Saksela, EMO J. 15, 290-298, 1996
A;Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (V
A;Reference number: S61795; MUID:96178224; PMID:8617204
A;Accession: S61795
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 70-419 <JOU>
A;Note: this sequence has been revised in reference S69207
A;Accession: S71443
A;Molecule type: protein
A;Residues: 'X', 104-120 <JOU>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and sp
A;Reference number: S69208
A;Accession: S69208
A;Molecule type: mRNA
A;Residues: 1-419 <LES>
A;Cross-references: EMBL:U43142; NID:gl1150988; PIDN:AAA85214.1; PID:gl1150989
R;Morris, J.C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01557
A;Accession: G02659
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-419 <MOR>
A;Cross-references: EMBL:U58111; NID:gl1373426; PIDN:AAB02909.1; PID:gl1373427
C;Genetics:
A;Gene: GDB:VEGFC; VRP
A;Cross-references: GDB:3890883; OMIM:601528
F;1-12/Domain: signal sequence #status predicted <SIG>
F;13-102/Domain: propeptide #status predicted <PRO>
F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>

Query Match 14.7%; Score 93; DB 2; Length 419;
Best Local Similarity 20.7%; Pred. No. 0.062;
Matches 38; Conservative 20; Mismatches 50; Indels 76; Gaps 8;

Qy 3 LDRLNDKAKRYSCTPRNYSVNIRELKLANVVF-PRCLLVQRCGNGC----- 50
Db 119 LKSIDNEWKTCQMPREVCIDVGKEFGVATNTFFKPCVSVYRCGCGCNSGLQCMNTST 178

Qy 51 -----CGTVNWRSCNCSKTV-KKYHEVLQ----- 75
Db 179 SYLSKTLFEITVPLSQGPKPVTISFANHSCRCNSKLDVYRQVHSIIRSLPATLPOCOA 238

Qy 76 -----FPGHFKR-----RGRAKTMALVDI-----QLDHHERCDCICSS 109
Db 239 ANKTCPTNMYNNHICRCLAQEDFMFSSDAGDSDTDFGDFHICGPNKELD-BETQCVCRA 297

Qy 110 --RP 111
Db 298 GLRP 301

RESULT 10
A37359
platelet-derived growth factor chain A precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 07-May-1999
C;Accession: A37359
R;Mercola, M.; Wang, C.; Kelly, J.; Brownlee, C.; Jackson-Grusby, L.; Stiles, C.; Bowen-
Dev. Biol. 138, 114-122, 1990
A;Title: Selective expression of PDGF A and its receptor during early mouse embryogenesis
A;Reference number: A37359; MUID:90169294; PMID:2155144
A;Accession: A37359
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A;Molecule type: mRNA
A;Residues: 1-196 <MER>
A;Cross-references: GB:M29464
C;Superfamily: platelet-derived growth factor

Query Match 14.1%; Score 89; DB 2; Length 196;
Best Local Similarity 26.8%; Pred. No. 0.081;
Matches 22; Conservative 18; Mismatches 32; Indels 10; Gaps 3;

Qy 31 ANVVFFPRCLLVQRCGNGCGGTNNRSCNCSKTVKKYHEVLQFEPGHFKRGRAKTM 90
Db 115 ANFLWPPCPVEVKRCTGCC-----NTSSVKQCPSRVHRSVKVAKVE--YVRKKPKLKE- 166

Qy 91 ALVDIQLDHHERCDCICSSRPP 112
Db 167 --VQVRLEEHLECACATSNLNP 186

RESULT 11
A48851
platelet-derived growth factor chain A precursor (version 2) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A48851; I51891
R;Katayose, D.; Ohe, M.; Yamauchi, K.; Ogata, M.; Shirato, K.; Fujita, H.; Shibahara, S.
Am. J. Physiol. 264, L100-L106, 1993
A;Title: Increased expression of PDGF A- and B-chain genes in rat lungs with hypoxic pul
A;Reference number: A48851; MUID:93191115; PMID:8447423
A;Accession: A48851
A;Molecule type: mRNA
A;Residues: 1-196 <KAT>
A;Cross-references: GB:D10106; NID:g220839; PIDN:BAA00987.1; PID:g220840
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBI:126515)
C;Superfamily: platelet-derived growth factor

Query Match 14.1%; Score 89; DB 2; Length 196;
Best Local Similarity 26.8%; Pred. No. 0.081;
Matches 22; Conservative 18; Mismatches 32; Indels 10; Gaps 3;

Qy 31 ANVVFFPRCLLVQRCGNGCGGTNNRSCNCSKTVKKYHEVLQFEPGHFKRGRAKTM 90
Db 115 ANFLWPPCPVEVKRCTGCC-----NTSSVKQCPSRVHRSVKVAKVE--YVRKKPKLKE- 166

Qy 91 ALVDIQLDHHERCDCICSSRPP 112
Db 167 --VQVRLEEHLECACATSNLNP 186

RESULT 12
B28964
platelet-derived growth factor chain A precursor splice form 2 - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: B28964; B42002; B28122
R;Bonthon, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.
Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988
A;Title: Platelet-derived growth factor A chain: gene structure, chromosomal location, a
A;Reference number: A28964; MUID:88144463; PMID:3422746
A;Accession: B28964
A;Molecule type: DNA
A;Residues: 1-196 <BON>
A;Cross-references: UNIPROT:P04085; GB:M21571; GB:J03638; GB:M19984; GB:M19985; GB:M1998
R;Bonthon, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Spoleman, F.
Genomics 13, 257-263, 1992
A;Title: Platelet-derived growth factor A chain: confirmation of localization of PDGFA t
A;Reference number: A42002; MUID:92307656; PMID:1612586
A;Accession: B42002
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 152-196 <BO2>
R;Rorsman, F.; Bywater, M.; Knott, T.J.; Scott, J.; Betsholtz, C.
Mol. Cell. Biol. 8, 571-577, 1988

R;Bonthonron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.
Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988
A;Title: Platelet-derived growth factor A chain: gene structure, chromosomal location, A
A;Reference number: A28964; MUID:88144463; PMID:3422746
A;Accession: A28964
A;Molecule type: DNA
A;Residues: 1-211 <BON>
A;Cross-references: UNIPROT:P04085; GB:M21571; GB:J03638; GB:M19984; GB:M19985; GB:M1999;
R;Takimoto, Y.; Kuramoto, A.
Biochim. Biophys. Acta 1222, 511-514, 1994
A;Title: Gene regulation by the 5'-untranslated region of the platelet-derived growth factor A
A;Reference number: S47564; MUID:94312450; PMID:7518695
A;Accession: S47564
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-21 <TAK>
R;Bonthonron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.
Genomics 13, 257-263, 1992
A;Title: Platelet-derived growth factor A chain: confirmation of localization of PDGFA
A;Reference number: A42002; MUID:92307656; PMID:1612586
A;Accession: A42002
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 152-211 <B02>
R;Betscholtz, C.; Johnson, A.; Heldin, C.H.; Westermark, B.; Lind, P.; Urdea, M.S.; Edö,
Nature 320, 695-699, 1986
A;Title: cDNA sequence and chromosomal localization of human platelet-derived growth fac
A;Reference number: A01379; MUID:86203630; PMID:3754619
A;Accession: A01379
A;Molecule type: mRNA
A;Residues: 1-211 <BET>
A;Cross-references: NID:G33795; NID:G3365; PIDN:CAA27421.1; PID:G35366
R;Experimental source: clonal glioma cell line U-343 MGac12.6, a tumor cell line
R;Hoppe, J.; Schumacher, L.; Eichner, W.; Weich, H.A.
FEBS Lett 223, 243-246, 1987
A;Title: The long 3'-untranslated regions of the PDGF-A and -B mRNAs are only distantly
A;Reference number: S00173; MUID:88030061; PMID:3666150
A;Accession: S00173
A;Molecule type: mRNA
A;Residues: 1-193, 'DVR', <HOP>
A;Cross-references: EMBL:X06374; NID:G35363; PIDN:CAA29677.1; PID:G35364
R;Rorsman, F.; Bywater, M.; Knott, T.J.; Scott, J.; Betscholtz, C.
Mol. Cell. Biol. 8, 571-577, 1988
A;Title: Structural characterization of the human platelet-derived growth factor A-chain.
A;Reference number: A28122; MUID:88174698; PMID:2832727
A;Accession: A28122
A;Molecule type: mRNA
A;Residues: 1-63, 'TRD', 67-211 <ROR>
A;Cross-references: GB:M20488
A;Note: the authors translated the codon ACA for residue 64 as Arg, CGT for residue 65
C;Comment: Platelet-derived growth factor, a potent mitogen for cells of mesenchymal or
C;Comment: A carboxyl-terminal propeptide may be removed from the precursor by proteoly
C;Genetics:
A;Gene: GDB:PDGFA
A;Cross-references: GDB:120266; OMIM:173430
A;Map position: 7p22-7p22
A;Introns: 21/3; 54/1; 89/1; 151/3; 194/1
C;Complex: homodimer; heterodimer (see PIR:PFHUG2)
C;Superfamily: platelet-derived growth factor
C;Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-86/Domain: propeptide #status predicted <PRO>
F;87-211/Product: platelet-derived growth factor chain A #status predicted <MAT>
F;158-162/Region: receptor binding #status predicted
F;96-140,129-177,133-179/Disulfide bonds: #status predicted
F;123/Disulfide bonds: interchain (to chain B-133 in heterodimeric form) #status predic
F;132/Disulfide bonds: interchain (to 132 in homodimeric form) #status predicted
F;132/Disulfide bonds: interchain (to chain B-124 in heterodimeric form) #status predic
F;132/Disulfide bonds: interchain (to 123 in homodimeric form) #status predicted
F;134/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.1%; Score 89; DB 1; Length 211;
Best Local Similarity 26.8%; Pred. No. 0.087;

A:Reference number: I51550; MUID:88321676; PMID:3413486
A:Accession: I51550
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-226 <MER>
A:Cross-references: UNIPROT:P13698; GB:M23237; NID:G214648; PIDN:AAA49927.1; PID:G214648
C:Superfamily: platelet-derived growth factor

Query Match 13.2%; Score 83; DB 2; Length 226;
Best Local Similarity 26.6%; Pred. No. 0.38;
Matches 21; Conservative 18; Mismatches 30; Indels 10; Gaps 3;

QY 31 ANVFFPRCLLVORCGGCGCTVNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTM 90
DB 120 ANFLVPPCPVEVKRTGCC-----NTSSVKQCPRIHRSVVKVKE--YVRKPKLKE- 171

QY 91 ALVDIQLDHHERCDCICSS 109

DB 172 --VLVRLEEHLECTTANS 188

RESULT 20

PFMSG

platelet-derived growth factor chain B precursor (sis) - mouse
N:Alternate names: PDGF-related transforming protein
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1992 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C:Accession: A39073

R:Bonthonron, D.T.; Sultan, P.; Collins, T.

Genomics 10, 287-292, 1991

A:Title: Structure of the murine c-sis proto-oncogene (Sis, PDGFB) encoding the B chain

A:Reference number: A39073; MUID:91257844; PMID:2045107

A:Accession: A39073

A:Molecule type: DNA

A:Residues: 1-241 <BON>

A:Cross-references: UNIPROT:P31240; GB:M64849; GB:M55394; NID:G192818; PIDN:AAA37485.1;

C:Genetics:

A:Gene: sis

C:Superfamily: platelet-derived growth factor

C:Keywords: glycoprotein; growth factor; platelet; proto-oncogene; transforming protein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-81/Domain: propeptide #status predicted <PRO>

F:82-190/Product: platelet-derived growth factor chain B #status predicted <MAT>

F:159-163/Region: receptor binding #status predicted

F:63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.5%; Score 79; DB 1; Length 241;

Best Local Similarity 30.1%; Pred. No. 1;

Matches 25; Conservative 12; Mismatches 34; Indels 12; Gaps 3;

QY 31 ANVFFPRCLLVORCGGCGCTVNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTM 90
DB 116 ANFLVPPCPVEVKRTGCC-----NNRNVCASQVQRPQVKIEIVRKPIFKKATV 170

QY 91 ALVDIQLDHHERCDC--ICSSRP 111

DB 171 TLED-----HLACKCETIVTPRP 188

Search completed: November 10, 2005, 09:36:11

Job time : 12.9317 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:21:06 ; Search time 51.0021 Seconds
(without alignments)
1134.561 Million cell updates/sec

Title: US-10-606-055-2_COPY_258_370

Perfect score: 631

Sequence: 1 VDLDRUNDKAKRYSTPRNY.....DIQLDHHERCDCICSSRPPR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	364	Q9BWV5	Q9bwv5 homo sapien
2	631	100.0	370	Q9GZP0	Q9gzp0 homo sapien
3	588	93.2	370	Q9A2I7	Q9a2i7 mus musculus
4	585	92.7	370	Q9EOT1	Q9eot1 rattus norv
5	511	81.0	300	Q6V9H4	Q6v9h4 oryctolagus
6	318.5	50.5	345	Q9NRA1	Q9nra1 homo sapien
7	318.5	50.5	345	Q9UL22	Q9ul22 homo sapien
8	315.5	50.0	345	Q9I946	Q9i946 gallus gall
9	312.5	49.5	345	Q9EQX6	Q9eqx6 rattus norv
10	311.5	49.4	345	Q9QV71	Q9qv71 m fallotein
11	311.5	49.4	345	Q8CI19	Q8ci19 mus musculus
12	305.5	48.4	345	Q9JHV8	Q9jnv8 mus musculus
13	202	32.0	258	Q8K429	Q8k429 rattus norv
14	106.5	16.9	176	Q7QFM8	Q7qfm8 anophelies g
15	104	16.5	326	1 VEGD RAT	Q35251 rattus norv
16	104	16.5	326	Q91ZEA	Q91ze4 rattus norv
17	102	16.2	194	Q6DC06	Q6dc06 brachydanio
18	102	16.2	354	1 VEGD_HUMAN	Q43915 homo sapien
19	100.5	15.9	148	1 VEGH_ORFN7	P52585 orf virus (
20	100	15.8	358	1 VEGD_MOUSE	P97946 mus musculus
21	99	15.7	149	Q6TVI8	Q6tv18 orf virus.
22	97.5	15.5	252	1 Q8QGD7	Q8qgd7 gallus gall
23	95.5	15.1	135	1 VEGB RAT	Q35485 rattus norv
24	95.5	15.1	186	Q6DGF3	Q6dgf3 rattus norv
25	95.5	15.1	207	1 VEGD_MOUSE	P49766 mus musculus
26	95	15.1	146	1 TXVE_BOTER	P6j936 bothrops er
27	95	15.1	304	2 Q9N4I3	Q9n4i3 caenorhabdi
28	94	14.9	152	2 Q8B571	Q8b571 pseudocowpo
29	94	14.9	213	1 PDGA_RABIT	P34007 oryctolagus
30	93	14.7	146	1 TXVE_BOTIN	Q90x24 bothrops in
31	93	14.7	251	2 Q90W23	Q90w23 gallus gall

32	93	14.7	419	1	VEGC_HUMAN	P49767 homo sapien
33	93	14.7	419	2	Q6FH59	Q6fh59 homo sapien
34	92.5	14.7	396	2	Q7T3I6	Q7t3i6 brachydanio
35	92	14.6	146	1	TXVE_BOTJA	Q90x23 bothrops la
36	92	14.6	405	2	Q9VM43	Q9vm43 drosophila
37	92	14.6	415	1	VEGC_MOUSE	P97953 mus musculus
38	92	14.6	415	2	Q91ZE3	Q91ze3 rattus norv
39	91.5	14.5	326	2	Q91ZH6	Q91zh6 meriones un
40	89	14.1	118	2	Q9CU96	Q9cu96 mus musculus
41	89	14.1	196	2	Q99L56	Q99l56 mus musculus
42	89	14.1	204	1	PDGA_RAT	P28576 rattus norv
43	89	14.1	211	1	PDGA_HUMAN	P04085 homo sapien
44	89	14.1	211	1	PDGA_MOUSE	P20033 mus musculus
45	89	14.1	211	2	Q6P7C3	Q6p7c3 rattus norv
46	89	14.1	211	2	Q7TPH7	Q7tph7 mus musculus
47	89	14.1	418	2	O57352	O57352 coturnix co
48	88.5	14.0	314	2	O5BLX1	O5blx1 drosophila
49	88.5	14.0	325	2	Q9VWP6	Q9vwp6 drosophila
50	88	13.9	149	2	Q9WVQ7	Q9wvq7 mesocricetu
51	87	13.8	420	2	Q9XS50	Q9xs50 bos taurus
52	86.5	13.7	195	2	Q9DE50	Q9de50 brachydanio
53	86.5	13.7	207	1	VEGB_BOVIN	Q9xs49 bos taurus
54	85.5	13.5	79	2	Q9FQ79	Q9fc79 musa acumin
55	85.5	13.5	132	2	Q772M8	Q772m8 orf virus s
56	85.5	13.5	132	2	Q9YMF3	Q9ymf3 orf virus.
57	85	13.5	148	2	O42571	O42571 xenopus lae
58	85	13.5	194	2	O42572	O42572 xenopus lae
59	84.5	13.4	79	2	Q6PML4	Q6pml4 populus bal
60	84.5	13.4	133	1	VEGH_ORFN2	P52584 orf virus (
61	84.5	13.4	146	1	TXVE_TRIFL	P67862 trimeresuru
62	84	13.3	137	2	Q6TVW8	Q6tvw8 orf virus.
63	83.5	13.2	80	2	O04107	O04107 oryza sativ
64	83.5	13.2	188	2	Q8TEV2	Q8tev2 homo sapien
65	83.5	13.2	207	1	VEGB_HUMAN	P49765 homo sapien
66	83.5	13.2	213	2	Q6DDJ9	Q6ddj9 xenopus lae
67	83	13.2	226	1	PDGA_XENLA	P13598 xenopus lae
68	83	13.2	346	2	Q674V2	Q674v2 podocoryne
69	82	13.0	191	1	VEGA_BITGA	P83906 bitis gabon
70	81.5	12.9	79	2	Q944W1	Q944w1 typha latif
71	81	12.8	77	1	Q75NH6	Q75nh6 pisum sativ
72	81	12.8	241	1	PDGB_SHEEP	Q95229 ovis aries
73	80.5	12.8	79	2	Q9AU16	Q9aul6 typha latif
74	80.5	12.8	344	2	Q9VY49	Q9vy49 drosophila
75	80	12.7	124	2	Q8XIQ7	Q8xiq7 clostridium
76	80	12.7	164	1	VEGA_CAVPO	P26617 cavia porce
77	80	12.7	194	2	Q90WK1	Q90wk1 gallus gall
78	80	12.7	198	2	Q90WK3	Q90wk3 gallus gall
79	80	12.7	211	2	Q90WK2	Q90wk2 gallus gall
80	79	12.5	219	2	Q8R3X9	Q8r3x9 mus musculus
81	79	12.5	241	1	PDGB_MOUSE	P31240 mus musculus
82	78.5	12.4	79	2	Q75NH9	Q75nh9 phaseolus a
83	78.5	12.4	79	2	Q75NI3	Q75ni3 phaseolus a
84	78.5	12.4	80	2	O22488	O22488 oryza sativ
85	78.5	12.4	110	1	TXVE_VIPLE	P82475 vipera lebe
86	78	12.4	108	2	Q8HY75	Q8hy75 ovis aries
87	78	12.4	211	2	Q9PUF7	Q9pu77 gallus gall
88	78	12.4	225	1	PDGB_RAT	Q05028 rattus norv
89	78	12.4	241	1	Q6P3C4	Q6p3c4 mus musculus
90	78	12.4	242	2	Q607I7	Q6q7i7 canis famil
91	78	12.4	297	1	Y622_TREPA	Y62222 treponema p
92	77.5	12.3	77	2	Q9ZNT5	Q9znt5 eichhornia
93	77	12.2	77	1	MT2_VICFA	Q41657 vicia faba
94	77	12.2	77	2	Q93X22	Q93x22 quercus sub
95	77	12.2	79	1	MT2_CICAR	Q39459 cicor ariet
96	77	12.2	79	2	Q9ZEV0	Q9zrv0 fagus sylv
97	77	12.2	118	2	Q9WZB1	Q9wzb1 ovis aries
98	77	12.2	136	2	Q8QCT9	Q8qct9 oryza sativ
99	77	12.2	136	2	Q8QGE8	Q8qge8 orf virus.
100	77	12.2	146	1	VEGA_SHEEP	P50412 ovis aries

ALIGNMENTS

```
RESULT 1
Q9BWV5
AC Q9BWV5 PRELIMINARY; PRT; 364 AA.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Iris-expressed growth factor short form (Platelet derived growth
factor D, isoform 2) (SCDGF-B).
GN Name=IEGF; Synonyms=PDGFB; ORFNames=UNQ1899;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RX MEDLINE=22103462; PubMed=12107412;
RA Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
RA Bouffard G., Smith D., Peterson K.;
RA "Expressed sequence tag analysis of adult human iris for the NEIBank
RT Project: steroid-response factors and similarities with retinal
RT pigment epithelium."
RL Mol. Vision 8:185-195 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Statchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX Strausberg R.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Eaton D., Foster B., Chui C., Crowley C., Curriel B., Deuel B., Dowd P.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandler R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RA "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270 (2003).
DR EMBL; AY027518; AAK20082.1; -
DR EMBL; BC030645; AAH30645.1; -
DR EMBL; AY359116; AAQ89474.1; -
```

```
DR PIR; JC7591; JC7591.
DR HSSP; Q9JJS8; LNT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD growth factor.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 364 AA; 42166 MW; 245C53E8DDEA9EAC CRC64;
Query Match 100.0%; Score 631; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VDLRLNDADKRYCTPRNYSVNIREELKLANVVFPRCLLVQRCCGCGCTVNRSC 60
Db 252 VDLRLNDADKRYCTPRNYSVNIREELKLANVVFPRCLLVQRCCGCGCTVNRSC 311
Qy 61 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPR 113
Db 312 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPR 364
RESULT 2
Q9GZP0 PRELIMINARY; PRT; 370 AA.
AC Q9GZP0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Spinal cord-derived growth factor-B (MSTP036) (Platelet-derived growth
factor D) (Iris-expressed growth factor long form).
GN Name=hSCDGF-B; Synonyms=IEGF, PDGFB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hanada T., Ui-Tai K., Imaki J., Miyata Y.;
RA "Molecular cloning of SCDGF-B, a novel growth factor homologous to
RT SCDGF/PDGF-C/fallorein."
RL Biochem. Biophys. Res. Commun. 280:733-737 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RA Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
RA LaRoche W.J., Jeffers M., McDonald W.F., Chillaakuru R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
RA Shimkets R.A., Rothberg J.M., Lichtenstein H.S.;
RA "PDGF D, A Novel Protease-Activated Growth Factor."
RL Nat. Cell Biol. 3:517-521 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11331881; DOI=10.1038/35074588;
RA Bergsten E., Urcela M., Li X., Pietras K., Ostman A., Heldin C.H.,
RA Aitala K., Eriksson U.;
RA "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
RT receptor."
RL Nat. Cell Biol. 3:512-516 (2001).
```



```

[5]
RN  SEQUENCE FROM N.A.
RP  TISSUE=iris;
RX  MEDLINE=22103462; PubMed=12107412;
RA  Wislow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
RA  Bouffard G., Smith D., Peterson K.;
RT  "Expressed sequence tag analysis of adult human iris for the NEIBank
RT  Project: steroid-response factors and similarities with retinal
RT  pigment epithelium.";
RL  Mol. Vision 8:185-195(2002).
DR  EMBL; AB033832; BAB18903.1; -
DR  EMBL; AF113216; AAG32827.1; -
DR  EMBL; AF335584; AAK38840.1; -
DR  EMBL; AF336376; AAK56136.1; -
DR  EMBL; AY027517; AAK20081.1; -
DR  PIR; JC7591; JC7591.
DR  HSP; O9JJS8; 1NTO.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0008083; P:growth factor activity; IEA.
DR  GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR  InterPro; IPR000859; CUB.
DR  InterPro; IPR000072; PD growth factor.
DR  InterPro; IPR010916; TORB_Box_N.
DR  Pfam; PF00431; CUB; 1.
DR  SMART; SM00042; CUB; 1.
DR  SMART; SM00141; PDGF; 1.
DR  PROSITE; PS01180; CUB; 1.
DR  PROSITE; PS0278; PDGF; 1.
DR  PROSITE; PS00430; TORB_DEPENDENT_REC.1; UNKNOWN 1.
SQ  SEQUENCE 370 AA; 42848 MW; D387F465E7BB7674 CRC64;

Query Match      100.0%; Score 631; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.7e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 VDLRLNDKAKYSCTPRNYNIREELKANVFPFRCLLVQRCGNGCGCTVNRST 60
DB  258 VDLRLNDKAKYSCTPRNYNIREELKANVFPFRCLLVQRCGNGCGCTVNRST 317
QY  61 CNSGKTVKKYHVEVLPFGPHIKRRGRKTMALVDIQLDHHRCDCICSSRP 113
DB  318 CNSGKTVKKYHVEVLPFGPHIKRRGRKTMALVDIQLDHHRCDCICSSRP 370

RESULT 3
Q92517
ID  Q92517 PRELIMINARY; PRT; 370 AA.
AC  Q92517; O9D16;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Platelet-derived growth factor D (Mus musculus 18-day embryo whole
DE  body cDNA, RIKEN full-length enriched library, clone:1110003109
DE  product:platelet-derived growth factor D).
GN  Name=Pdgid;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
[1]
RN  SEQUENCE FROM N.A.
RP  STRAIN=BALB/c;
RX  MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
RA  LeRochele W.J., Jeffers M., McDonald W.F., Chillaakuru R.A.,
RA  Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA  Burgess C.E., Fernandez E., Degler L.L., Rittman B., Shinkets J.,
RA  Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
RT  "PDGF D, A Novel Protease-Activated Growth Factor.";
RL  Nat. Cell Biol. 3:517-521(2001).
[2]
RN  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=Whole body;
RX  MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX  MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

```

```

RA  Carninci P., Hayashizaki Y.;
RT  "High-efficiency full-length cDNA cloning.";
RL  Meth. Enzymol. 303:19-44(1999).
[3]
RN  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=Whole body; DOI=10.1038/35055500;
RX  MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA  RIKEN FANTOM Consortium;
RT  "Functional annotation of a full-length mouse cDNA collection.";
RL  Nature 409:685-690(2001).
[4]
RN  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=Whole body;
RA  The FANTOM Consortium,
RA  the RIKEN Genome Exploration Research Group Phase I & II Team;
RT  "Analysis of the mouse transcriptome based on functional annotation of
RT  60,770 full-length cDNAs.";
RL  Nature 420:563-573(2002).
[5]
RN  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=Whole body;
RX  MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA  Carninci P., Shibata Y., Hayatsu N., Suehara Y., Shibata K., Itoh M.,
RA  Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT  "Normalization and subtraction of cap-trapper-selected cDNAs to
RT  prepare full-length cDNA libraries for rapid discovery of new genes.";
RL  Genome Res. 10:1617-1630(2000).
[6]
RN  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=Whole body; DOI=10.1101/gr.152600;
RX  MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA  Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA  Konno H., Akiyama Y., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hazada A.,
RA  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA  Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA  Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT  "RIKEN integrated sequence analysis (RISA) system-384-format
RT  sequencing pipeline with 384 multicapillary sequencer.";
RL  Genome Res. 10:1757-1771(2000).
[7]
RN  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=Whole body;
RA  Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA  Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA  Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA  Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA  Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA  Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA  Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA  Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA  Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA  Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA  Muramatsu M., Hayashizaki Y.;
RL  Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF335583; AAK38839.1; -
DR  EMBL; AK003359; BAB2735.2; -
DR  HSP; O9JJS8; 1NTO.
DR  MGD; MGI:1919035; Pdgid.
DR  GO; GO:0005615; C:extracellular space; TAS.
DR  GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR  Pfam; PF00431; CUB; 1.
DR  SMART; SM00042; CUB; 1.
DR  SMART; SM00141; PDGF; 1.
DR  PROSITE; PS01180; CUB; 1.
DR  PROSITE; PS0278; PDGF; 1.
SQ  SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFFE CRC64;

Query Match      93.2%; Score 588; DB 2; Length 370;
Best Local Similarity 90.3%; Pred. No. 2e-56;
Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

```

```
QY 1 VDLRLNDADKRYSTPRNYSVNIREEELKLANVFFPRCLLVQRCGCGGVNWRSC 60
Db 258 VDLRLNDVVKRYSTPRNHSVNLREELKLTNAVFFPRCLLVQRCGCGGVNWKSC 317
QY 61 CMSGKTVKKYHEVLQFEPGHIIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113
Db 318 CSSGKTVKKYHEVLKFEFGHFKRRGKAKNMALVDIQLDHHERCDCICSSRPPR 370

RESULT 4
Q9EQT1 ID Q9EQT1 PRELIMINARY; PRT; 370 AA.
AC Q9EQT1;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Spinal-cord derived growth factor-B.
GN Name=rSCDGF-B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hamada T., Ui-Tei K., Inaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
RT SCDGF/PDGF-C/fallotectin.";
RL Biochem. Biophys. Res. Commun. 280:733-737 (2001).
DR EMBL; AB052170; BAB18920.1; -.
DR PIR; JC7592; JC7592.
DR HSP; O9UCV4; INZI.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; F:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 370 AA; 42809 MW; 7B58A251F679BF73 CRC64;

Query Match 92.7%; Score 585; DB 2; Length 370;
Best Local Similarity 89.4%; Pred. No. 4.4e-56;
Matches 101; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDLRLNDADKRYSTPRNYSVNIREEELKLANVFFPRCLLVQRCGCGGVNWRSC 60
Db 258 VDLRLNDVVKRYSTPRNHSVNLREELKLTNAVFFPRCLLVQRCGCGGVNWKSC 317
QY 61 CMSGKTVKKYHEVLQFEPGHIIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113
Db 318 CSSGKTVKKYHEVLKFEFGHFKRRGKAKNMALVDIQLDHHERCDCICSSRPPR 370

RESULT 5
Q6V9H4 ID Q6V9H4 PRELIMINARY; PRT; 300 AA.
AC Q6V9H4;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Iris-expressed growth factor (Fragment).
GN Name=PDGFD;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX Ray S., Wistow G.;
```

```
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY347260; AAQ24382.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; F:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
FT NON TER 1 300
FT NON TER 300 300
SQ SEQUENCE 300 AA; 34616 MW; 716C873C9C01C0C6 CRC64;

Query Match 81.0%; Score 511; DB 2; Length 300;
Best Local Similarity 91.9%; Pred. No. 5.1e-48;
Matches 91; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDLRLNDADKRYSTPRNYSVNIREEELKLANVFFPRCLLVQRCGCGGVNWRSC 60
Db 202 VDLRLNDADKRYSTPRNYSVNIREEELKLTNAVFFPRCLLVQRCGCGGVNWKSC 261
QY 61 CMSGKTVKKYHEVLQFEPGHIIKRRGRKTMALVDIQLD 99
Db 262 CSSGKTVKKYHEVLKFEFGHFKRRNRAKNMALVDIQLDH 300

RESULT 6
Q9NRA1 ID Q9NRA1 PRELIMINARY; PRT; 345 AA.
AC Q9NRA1;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RX MEDLINE=20268201; PubMed=10806482; DOI=10.1038/35010579;
RA Li X., Ponten A., Aase K., Karlsson L., Abramson A., Uetela M.,
RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
RA Betsholtz C., Haldin C.-H., Alitalo K., Ostman A., Eriksson U.;
RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-
RT receptor.";
RL Nat. Cell Biol. 2:302-309 (2000).
CC -1. SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF244813; AAF80597.1; -.
DR HSP; Q9JUS9; INT0.
DR Genew; HGNC:8801; PDGFC.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; F:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 50.5%; Score 318.5; DB 2; Length 345;
Best Local Similarity 53.3%; Pred. No. 1e-26;
Matches 57; Conservative 14; Mismatches 33; Indels 3; Gaps 1;
```

```
QY 1 VLDRLNDADKRYSCPTPRNYSVNIIRBELKLANVVFPPRCLLVORCGNCGCGTVNWRSC 60
DB 236 VDLNLLTEEVRLSYCTPRNFSVIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQ 295
QY 61 CNSGKTVKYYKHEVLOPEPGHKKRGRKTMALVDIQLDHHERCDCIC 107
DB 296 CVPSKTVKYYKHEVLOLRP----KTGVRGLHKSILTDVALEHHEECDCVC 339

RESULT 7
Q9UL22 PRELIMINARY; PRT; 345 AA.
ID Q9UL22;
AC Q9UL22;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Secretory growth factor-like protein fallotelin (Spinal cord-derived
DE growth factor) (Platelet-derived growth factor C) (VEGF-E).
GN Name-hSCDGF; Synonyms=PDGFC; ORNames=UNQ174;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=20461776; PubMed=11004490; DOI=10.1016/S0167-4781(00)00066-X;
RA Tsai Y.J., Lee R.K., Lin S.P., Chen Y.H.;
RT "Identification of a novel platelet-derived growth factor-like gene,
RT fallotelin, in the human reproductive tract.";
RL Biochim. Biophys. Acta 1492:196-202(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347863; PubMed=11397552; DOI=10.1074/jbc.M101056200;
RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
RA Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
RT "Platelet-derived factor C (PDGF-C), a novel growth factor that
RT binds to PDGF alpha and beta receptor.";
RL J. Biol. Chem. 276:27406-27414(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiewand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AF091434; AAF00049.1; -
DR EMBL; AB033831; BAB03266.1; -
DR EMBL; AF260738; AAK51637.1; -
DR EMBL; AY358493; AAK88857.1; -
DR HSSP; Q9JJS8; INT0.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0008083; F:growth factor activity; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR InterPro; IPR000859; CUB.
```

```
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 50.5%; Score 318.5; DB 2; Length 345;
Best Local Similarity 53.3%; Pred. No. 1e-26;
Matches 57; Conservative 14; Mismatches 33; Indels 3; Gaps 1;

QY 1 VLDRLNDADKRYSCPTPRNYSVNIIRBELKLANVVFPPRCLLVORCGNCGCGTVNWRSC 60
DB 236 VDLNLLTEEVRLSYCTPRNFSVIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQ 295
QY 61 CNSGKTVKYYKHEVLOPEPGHKKRGRKTMALVDIQLDHHERCDCIC 107
DB 296 CVPSKTVKYYKHEVLOLRP----KTGVRGLHKSILTDVALEHHEECDCVC 339

RESULT 8
Q9I946 PRELIMINARY; PRT; 345 AA.
ID Q9I946;
AC Q9I946;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=SCDGF;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Spinal cord;
RX MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
CC -I- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AB033829; BAB03265.1; -
DR HSSP; Q9JJS8; INT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF 2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 50.0%; Score 315.5; DB 2; Length 345;
Best Local Similarity 52.8%; Pred. No. 2.2e-26;
Matches 57; Conservative 16; Mismatches 30; Indels 5; Gaps 2;

QY 1 VLDRLNDADKRYSCPTPRNYSVNIIRBELKLANVVFPPRCLLVORCGNCGCGTVNWRSC 60
DB 236 VDLNLLKEVRLSYCTPRNFSVIRBELKRTDTIFWPLCLLVKRCGNCACCHQNCNECQ 295
QY 61 CNSGKTVKYYKHEVLOPEPGHKKRGRKTMALVDIQLDHHERCDCIC 107
DB 296 CIPTKTVKYYKHEVLOLRP----RSRGRGLHKSILTDVPLEHHEECDCVC 339
```

```
RESULT 9
O3EQX6
ID Q9EQX6 PRELIMINARY; PRT; 345 AA.
AC Q9EQX6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=rscdgf;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hamada T., Ui-Tei K., Inaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
RT SCDGF/PDGF-C/fallotain.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AB033830; BAB19969.1; -.
DR HSP; Q9JJS8; INTO.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; F:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF.2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;

Query Match 49.5%; Score 312.5; DB 2; Length 345;
Best Local Similarity 54.2%; Pred. No. 4.8e-26;
Matches 58; Conservative 15; Mismatches 31; Indels 3; Gaps 2;

QY 1 VDLRLDNDKAYSCYTPNYSVNIIEELKLANVFFPRCLLVORCGNGCGTVMWRSCT 60
Db 236 VNLNLKBEVLLKSCYTPNFSVIREELKRTDTIFWPGCLLVKRCGGNACCLHNCNECQ 295

QY 61 CNSGKTVMKYHEVLQFEPGHKIKRRGAKTMAVLDIQLDHERCDIC 107
Db 296 CVPRKVTKYHEVLQLRP-KIGVKGLHK--SLTDVALEHHECDVCV 339

RESULT 10
Q9QY71
ID Q9QY71 PRELIMINARY; PRT; 345 AA.
AC Q9QY71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Fallotain (Platelet-derived growth factor C) (Mus musculus adult male
DE cecum cDNA, RIKEN full-length enriched library, clone:9130403O08
DE product:platelet-derived growth factor, C polypeptide, full insert
DE sequence) (Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-
DE length enriched library, clone:A730022G11 product:platelet-derived
DE growth factor, C polypeptide, full insert sequence) (Mus musculus 15
DE days embryo head cDNA, RIKEN full-length enriched library,
DE clone:D93001M08 product:platelet-derived growth factor, C
DE polypeptide, full insert sequence).
GN Name=Pdgfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
```

```
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,
RA Gilbertson D., West J., O'Hara P.J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RL Nature 420:563-573(2002).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RA Adachi J., Aizawa K., Akimura T., Akakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirokane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tonaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
```

```

[2]
RN      SEQUENCE FROM N.A.
RP      STRAIN=CZECH II; TISSUE=Mammary tumor;
RC      Strausberg R.;
RL      Submitted (SEP-2002) to the ENBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: belongs to the PDGF/VEGF growth factor family.
DR      ENBL; BC037696; AAH37696.1; -.
DR      HSSP; Q9JJJ8; 1NT0.
DR      MGD; MGI:1859631; Pdgcfc.
DR      GO; GO:0005615; C:extracellular space; TAS.
DR      GO; GO:0005163; P:platelet-derived growth factor receptor bin. .; IDA.
DR      GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR      GO; GO:0005073; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR      GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR      InterPro; IPR000859; CUB.
DR      InterPro; IPR00072; PD_growth_factor.
DR      Pfam; PF00431; CUB; 1.
DR      Pfam; PF00341; PDGF; 1.
DR      SMART; SM00042; CUB; 1.
DR      SMART; SM00141; PDGF; 1.
DR      PROSITE; PS01180; CUB; 1.
DR      PROSITE; PS0278; PDGF.2; 1.
KW      Growth factor; Mitogen_2.
SQ      SEQUENCE 345 AA; 38741 MW; 9A58A05C6C0E9614 CRC64;

Query Match          49.4%; Score 311.5; DB 2; Length 345;
Best Local Similarity 52.3%; Pred. No. 6.2e-26;
Matches 56; Conservative 15; Mismatches 33; Indels 3; Gaps 1

Qy      1 VDLRLNDKAKRYSCYTPRNYSVNTRBELKLANVVFPRCLLVORCGNGCCGTVNWRSC 60
Db      236 VNLNLKLEKVLKSYTPRNFVSIRBELKRTDTITFWPGCLLVKRCGNCACCLHNCNEQ 295

Qy      61 CNSGKTVKVKYHEVQLQFEPGHTKRRGRAKTWALVDIQLDHRHCDCIC 107
Db      296 CVPRKTVTKYHEVQLQRP---KTGVKGLHKSLTDVALEHHECDVC 339

RESULT 12
Q9JHV8
ID      Q9JHV8      PRELIMINARY;      PRT;      345 AA.
AC      Q9JHV8;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      Platelet-derived growth factor C.
GN      Names=PDgfc;
OC      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RN      SEQUENCE FROM N.A.
RC      STRAIN=Swiss-Webster/NIH;
RX      MEDLINE=20417814; PubMed=10960785; DOI=10.1016/S0925-4773(00)00425-1;
RA      Ding H., Wu X., Kim I., Tam P.P.L., Koh G.-Y., Nagy A.;
RT      "The mouse pdgfc gene: dynamic expression in embryonic tissues during
RT      organogenesis.";
RL      Mech. Dev. 96:209-213 (2000).
DR      ENBL; AF286725; AAF91483.1; -.
DR      HSSP; Q9JJJ8; 1NT0.
DR      MGD; MGI:1859631; Pdgcfc.
DR      GO; GO:0005615; C:extracellular space; TAS.
DR      GO; GO:0005163; P:platelet-derived growth factor receptor bin. .; IDA.
DR      GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR      GO; GO:0005073; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR      GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR      InterPro; IPR000859; CUB.
DR      InterPro; IPR00072; PD_growth_factor.
DR      Pfam; PF00431; CUB; 1.
DR      SMART; SM00042; CUB; 1.
DR      SMART; SM00141; PDGF; 1.
DR      PROSITE; PS01180; CUB; 1.

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:20:26 ; Search time 177.723 Seconds
(without alignments)
805.195 Million cell updates/sec

Title: US-10-606-055-2

Perfect score: 1994

Sequence: 1 MHRLIFVYTYLCANFCSCRD.....DIQLDHERCDCICSSRPPR 370

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1994	100.0	370	3	Aay96864 SEQ. ID.
2	1994	100.0	370	3	Aab48653 Human gro
3	1994	100.0	370	3	Aay71130 Human Pla
4	1994	100.0	370	4	Aab60888 Human VEG
5	1994	100.0	370	4	Aau00704 Human PDG
6	1994	100.0	370	4	Aau00698 Human FCT
7	1994	100.0	370	4	Aag65601 Human zve
8	1994	100.0	370	4	Aae00999 Human zve
9	1994	100.0	370	4	Aab85529 Human sec
10	1994	100.0	370	5	Aae15819 Human LP8
11	1994	100.0	370	5	Aab79643 Human FCT
12	1994	100.0	370	5	Abg92893 Human VEG
13	1994	100.0	370	5	Aab47891 Human zve
14	1994	100.0	370	5	Abb79588 Human zve
15	1994	100.0	370	5	Abg78502 Human FCT
16	1994	100.0	370	5	Abg76575 Human sec
17	1994	100.0	370	5	Abg64733 Human alb
18	1994	100.0	370	5	Abp51640 Human zve
19	1994	100.0	370	6	Abu72430 Human gro
20	1994	100.0	370	6	Abg76397 Human gro
21	1994	100.0	370	6	Abb80134 PDGF-D. 6
22	1994	100.0	370	6	Abbr43944 Human PDG
23	1994	100.0	370	7	Aae38476 Human pla
24	1994	100.0	370	7	Abw02697 Human zve
25	1994	100.0	370	7	Adg47746 Human zve

26	1994	100.0	370	8	ADJ32755 Human zve
27	1994	100.0	370	8	ADL78000 Albumin f
28	1994	100.0	370	8	ADL67182 Human zve
29	1994	100.0	370	8	ADL18360 Human zve
30	1994	100.0	370	8	ADM57643 Human FCT
31	1994	100.0	370	8	ADO20113 Human PRO
32	1994	100.0	370	8	ADR31427 Human Pla
33	1989	99.7	370	5	AAE15845 Human LP8
34	1989	99.7	370	5	AAE15849 Human LP8
35	1988	99.7	370	4	AAB85547 Human sec
36	1988	99.7	370	5	AAE15847 Human LP8
37	1988	99.7	370	5	AAE15844 Human LP8
38	1988	99.7	370	5	AAE15846 Human LP8
39	1988	99.7	370	5	AAE15851 Human LP8
40	1988	99.7	370	5	ABG76593 Human sec
41	1988	99.7	370	5	ABG64732 Human alb
42	1988	99.7	370	8	ADL77999 Albumin f
43	1986	99.6	370	5	AAE15848 Human LP8
44	1995	99.5	370	5	ABG78507 Human FCT
45	1984	99.5	370	5	AAE15850 Human LP8
46	1982	99.4	368	7	ADG65193 Cell prol
47	1949	97.7	364	4	AAU12264 Human PRO
48	1949	97.7	364	5	AAE15820 Human LP8
49	1949	97.7	364	5	ABB84973 Human PRO
50	1949	97.7	364	5	ABB95579 Human ang
51	1949	97.7	364	6	ABO17708 Novel hum
52	1949	97.7	364	6	ABU80962 Human PRO
53	1949	97.7	364	6	ABU66662 Human PRO
54	1949	97.7	364	6	ABU59743 Novel sec
55	1949	97.7	364	6	ABO24933 Human sec
56	1949	97.7	364	6	ABU66938 Human sec
57	1949	97.7	364	6	ADA45705 Novel hum
58	1949	97.7	364	6	ADA76136 Human PRO
59	1949	97.7	364	6	ADA18786 Human PRO
60	1949	97.7	364	6	ADA61409 Homo sapi
61	1949	97.7	364	6	ADB19194 Novel hum
62	1949	97.7	364	6	ADB27735 Human PRO
63	1949	97.7	364	6	ADA86214 Novel hum
64	1949	97.7	364	6	ADB15778 Human PRO
65	1949	97.7	364	6	ADA47564 Human PRO
66	1949	97.7	364	6	ADA67359 Human PRO
67	1949	97.7	364	6	ADB30366 Human PRO
68	1949	97.7	364	6	ADA85662 Novel hum
69	1949	97.7	364	6	ADA96874 Human PRO
70	1949	97.7	364	6	ADA79178 Human PRO
71	1949	97.7	364	6	ADA87317 Novel hum
72	1949	97.7	364	6	ADB16519 Human PRO
73	1949	97.7	364	6	ADA91611 Novel hum
74	1949	97.7	364	6	ADB14674 Human PRO
75	1949	97.7	364	6	ADB18635 Novel hum
76	1949	97.7	364	6	ADA93850 Human PRO
77	1949	97.7	364	6	ADB19746 Novel hum
78	1949	97.7	364	6	ADB13058 Human PRO
79	1949	97.7	364	6	ABO43241 Novel hum
80	1949	97.7	364	6	ADA74312 Human PRO
81	1949	97.7	364	6	ADA24545 Human PRO
82	1949	97.7	364	6	ADA82069 Human PRO
83	1949	97.7	364	6	ADA75032 Human PRO
84	1949	97.7	364	6	ADA85110 Novel hum
85	1949	97.7	364	6	ADA84558 Novel hum
86	1949	97.7	364	6	ADB29814 Human PRO
87	1949	97.7	364	6	ADA80342 Human PRO
88	1949	97.7	364	6	ADA75584 Human PRO
89	1949	97.7	364	6	ADA46809 Human PRO
90	1949	97.7	364	6	ADB25105 Human PRO
91	1949	97.7	364	6	ADA93281 Human PRO
92	1949	97.7	364	6	ADB26631 Human PRO
93	1949	97.7	364	6	ADB30918 Human PRO
94	1949	97.7	364	6	ADA60846 Homo sapi
95	1949	97.7	364	6	ADB23993 Human PRO
96	1949	97.7	364	6	ADA96322 Human PRO
97	1949	97.7	364	6	ADA80894 Human PRO
98	1949	97.7	364	6	ADA95770 Human PRO

99 1949 97.7 364 6 ADB26079 Human PRO
100 1949 97.7 364 6 ADB21564 Novel hum

ALIGNMENTS

RESULT 1
AAAY96864
ID AAAY96864 standard; protein; 370 AA.

AC AAAY96864;
DT 26-SEP-2000 (first entry)
XX
DE SEQ. ID. 37 from WO0034474.

XX Vascular endothelial growth factor; homologue; zveg3; CUB domain;
KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;
KW chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;
KW vulnery.

XX Homo sapiens.
OS
PN WO200034474-A2.
XX
PD 15-JUN-2000.

XX 07-DEC-1999; 99WO-US028968.
XX
PR 07-DEC-1998; 98US-00207120.
PR 06-JUL-1999; 99US-0142578P.
PR 21-OCT-1999; 99US-0161653P.
PR 12-NOV-1999; 99US-0165255P.

XX (ZYMO) ZYMOGENETICS INC.

XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
PI Gilbertson DG, West JW;
XX
DR WPI; 2000-423420/36.
DR N-PSDB; AAA51541.

XX Novel zveg3 polypeptides and nucleotides encoding them useful for
PT stimulating growth of smooth muscle cells and fibroblasts comprising an
PT epitope bearing portion of a specific amino acid sequence.

XX Disclosure; Page 164-165; 173pp; English.

XX Polypeptides comprising an epitope-bearing portion human or murine ZVEGF3
CC (vascular endothelial growth factor homologue) are claimed. The growth
CC factors comprise a growth factor domain and a CUB domain (generic
CC sequence motifs are shown in AA96859 and AA96860). The growth factor
CC domain is characterized by an arrangement of cysteine residues and beta-
CC strands that is characteristic of the "cysteine knot" structure of the
CC platelet-derived growth factor (PDGF) family. The CUB domain shows
CC homology to CUB domains in neuropilins, human bone morphogenetic protein-
CC 1, porcine seminal plasma protein, bovine acidic seminal fluid protein
CC and Xenopus laevis tolloid-like protein. Structural analysis and homology
CC predict that ZVEGF3 polypeptides complex with a second polypeptide to
CC form multimeric proteins. The human zveg3 gene has been mapped to
CC chromosome 4q28.3. ZVEGF3 is useful for stimulating the growth of
CC fibroblasts or smooth muscle cells, for activating cell surface PDGF-
CC alpha receptor and for inhibiting PDGF-alpha receptor mediated cellular
CC processes. ZVEGF3 is useful for regulating (post-development) organ
CC growth, regeneration and maintenance, as well as tissue maintenance and
CC repair processes. ZVEGF3 antagonists are useful for treating cancer,
CC rheumatoid arthritis, diabetic retinopathy, ischemic limb disease,
CC peripheral vascular disease, myocardial ischemia, vascular intimal
CC hyperplasia, atherosclerosis, wound healing, chronic liver disease and
CC haemangioma formation. ZVEGF3 can also be used to modulate neurite growth
CC and development of the nervous system, and for treating neurodegenerative

CC diseases
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFYVYTLICANFCSCRDTSATPQASIKALNANLRRDESNNHLDLYRDETIQVKG 60
|||
Db 1 MHRLLFYVYTLICANFCSCRDTSATPQASIKALNANLRRDESNNHLDLYRDETIQVKG 60
|||

QY 61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
|||
Db 61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
|||

QY 121 ETSTIIRGRWCGHKVEPPRIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
|||
Db 121 ETSTIIRGRWCGHKVEPPRIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
|||

QY 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKTAEDTVEDLLKYFNPSQEDLENNY 240
|||
Db 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKTAEDTVEDLLKYFNPSQEDLENNY 240
|||

QY 241 LDTPRYGRSYHDKRSKVDLRLNDLNDKRYSCPTPNYSVNIRESLKLNVVFFPRCLLVQ 300
|||
Db 241 LDTPRYGRSYHDKRSKVDLRLNDLNDKRYSCPTPNYSVNIRESLKLNVVFFPRCLLVQ 300
|||

QY 301 RCGNCGCGTVNWSCTCNSGKTVKHYEVLQFEPGHIKRRGAKTVALVDIQLDHHERC 360
|||
Db 301 RCGNCGCGTVNWSCTCNSGKTVKHYEVLQFEPGHIKRRGAKTVALVDIQLDHHERC 360
|||

QY 361 DCICSSRRPPR 370
|||
Db 361 DCICSSRRPPR 370
|||

RESULT 2
AAB48653
ID AAB48653 standard; protein; 370 AA.
XX
AC AAB48653;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human growth factor homologue zveg4, SEQ ID NO:2.
XX
KW Human; zveg4; growth factor homologue; VEGF/PDGF family; CUB domain;
KW PDGF-like activity; mitogenic; osteogenic; neovascularisation;
KW tissue repair; proliferation; differentiation; liver damage;
KW neuroregenerative; Alzheimer's disease; multiple sclerosis;
KW periodontal disease; bone fracture; wound healing; ischaemia;
KW immunomodulation; hepatic; chromosome 11q22.3-23.1.
XX
OS Homo sapiens.
PN WO200066736-A1.
XX
PD 09-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-US040047.
XX
PR 03-MAY-1999; 99US-00304216.
PR 10-NOV-1999; 99US-0164463P.
PR 04-FEB-2000; 2000US-0180169P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
XX
DR WPI; 2000-687541/67.
DR N-PSDB; AAC81555.
XX

PA (CURA-) CURAGEN CORP.
XX Shinkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
PI Jeffers M;
XX WPI; 2001-316172/33.
DR N-PSDB; AAS04492.
XX Novel growth factor polypeptides termed as FCTR polypeptides, useful for
PT treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
PT wound healing and neuronal disorders.
XX
PS Disclosure; Fig 13; 171pp; English.
XX
CC The sequence represents a protein related to bone morphogenetic protein-1
CC (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived
CC growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1,
CC VEGF-E and PDGF are referred to as FCTR peptides and nucleic acids.
CC FCTR proteins are useful for treating or preventing a disorder
CC associated with aberrant expression, aberrant processing, or aberrant
CC physiological interactions of the proteins in a mammal, where the
CC disorder is characterised by insufficient or ineffective growth of a cell
CC or a tissue, e.g. hyperplasia or neoplasia. The peptides and their
CC associated nucleic acids are useful for both promoting and inhibiting
CC growth of cells and tissues and in treatment of cancer, anaemia,
CC leukopenia, baldness, for treating cardiovascular and fibrotic disorders,
CC diabetic ulcers, obesity, infectious diseases, hyperproliferative and
CC dysproliferative disorders, neurodegenerative disorders, osteoarthritis,
CC inflammatory disorders, Graft versus host disease, coagulation disorders
CC such as haemophilia, and neural disorders including Parkinson's disease,
CC Alzheimer's disease, multiple sclerosis, Huntington's disease,
CC amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
CC and epilepsy
XX
SQ Sequence 370 AA;
Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLDLYRDETIQVKG 60
Db 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLDLYRDETIQVKG 60
QY 61 NGYVSPRPNSYPNRLLLTWRLHSEENTRIQLVFDNQGLBEAENDICRYDFVEVEDIS 120
Db 61 NGYVSPRPNSYPNRLLLTWRLHSEENTRIQLVFDNQGLBEAENDICRYDFVEVEDIS 120
QY 121 ETSITIRGMCVGHKEVPPRIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSITIRGMCVGHKEVPPRIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
QY 181 TWVESVTSISGVSNPSVPTTLIADALDKKIAEFDFVEDLLKYFNESQWEDLENNY 240
Db 181 TWVESVTSISGVSNPSVPTTLIADALDKKIAEFDFVEDLLKYFNESQWEDLENNY 240
QY 241 LQTPRYGRSYHDKRSKVDLRDLNDKRYSTCPNYSVNIREELKLANVFPFRCCLVQ 300
Db 241 LQTPRYGRSYHDKRSKVDLRDLNDKRYSTCPNYSVNIREELKLANVFPFRCCLVQ 300
QY 301 RCGNCGCGCTVNRSTCNSGKTVKYKHEVLPQEPGHIKRRGRKTMALVDIQLDHERC 360
Db 301 RCGNCGCGCTVNRSTCNSGKTVKYKHEVLPQEPGHIKRRGRKTMALVDIQLDHERC 360
QY 361 DCICSRPPR 370
Db 361 DCICSRPPR 370

RESULT 6

AAU00698

ID AAU00698 standard; protein; 370 AA.

XX

AC AAU00698;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human FCTR1 protein present in clone 30664188.0.99.
XX
KW Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;
KW VEGF-E; platelet derived growth factor; PDGF; FCTR; hyperplasia; cancer;
KW neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;
KW fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;
KW dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;
KW inflammatory disorder; Graft versus host disease; coagulation;
KW haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;
KW multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
KW peripheral neuropathy; acute brain injury.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23 /note= "Signal peptide"
FT Protein 24..370 /note= "Mature FCTR1"
FT Domain 53..167 /note= "CUB domain"
FT Domain 272..306 /note= "PDGF domain"
FT Modified-site 276 /note= "N-linked glycosylation site"
FT Domain 302..365 /note= "Metallothionein domain"
FT Domain 350..362 /note= "PDGF domain"
XX
PN WO200125437-A2.
XX
PD 12-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US027671.
XX
PR 07-OCT-1999; 99US-0158083P.
PR 13-OCT-1999; 99US-0159231P.
PR 04-JAN-2000; 2000US-0174485P.
PR 03-MAR-2000; 2000US-0186707P.
PR 10-MAR-2000; 2000US-0188250P.
PR 08-AUG-2000; 2000US-0223879P.
PR 12-SEP-2000; 2000US-00662783.
PR 20-SEP-2000; 2000US-0234082P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
PI Jeffers M;
XX
XX WPI; 2001-316172/33.
DR N-PSDB; AAS04492.
XX
XX Novel growth factor polypeptides termed as FCTR polypeptides, useful for
PT treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
PT wound healing and neuronal disorders.
XX
PS Claim 1; Fig 1; 171pp; English.
XX
CC The sequence represents a protein related to bone morphogenetic protein-1
CC (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived
CC growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1,
CC VEGF-E and PDGF are referred to as FCTR peptides and nucleic acids.
CC FCTR proteins are useful for treating or preventing a disorder
CC associated with aberrant expression, aberrant processing, or aberrant
CC physiological interactions of the proteins in a mammal, where the
CC disorder is characterised by insufficient or ineffective growth of a cell
CC or a tissue, e.g. hyperplasia or neoplasia. The peptides and their
CC associated nucleic acids are useful for both promoting and inhibiting

CC growth of cells and tissues and in treatment of cancer, anaemia,
CC leukopenia, baldness, for treating cardiovascular and fibrotic disorders,
CC diabetic ulcers, obesity, infectious diseases, hyperproliferative and
CC dysproliferative disorders, neurodegenerative disorders, osteoarthritis,
CC inflammatory disorders, Graft versus host disease, coagulation disorders
CC such as haemophilia, and neural disorders including Parkinson's disease,
CC Alzheimer's disease, multiple sclerosis, Huntington's disease,
CC amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
CC and epilepsy
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLI FVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRRDET IQVG 60
Db 1 MHRLI FVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRRDET IQVG 60

Qy 61 NGYVQSRPFNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLAEAEENDICRYDFVEVEDIS 120
Dy 61 NGYVQSRPFNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLAEAEENDICRYDFVEVEDIS 120

Qy 121 ETSIIIRGWCCHKEVPPRIKSRTNQIKITPKSDDYFVAKGPKFIYYSLLLEDFOFAAASE 180
Dy 121 ETSIIIRGWCCHKEVPPRIKSRTNQIKITPKSDDYFVAKGPKFIYYSLLLEDFOFAAASE 180

Qy 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFPNPSQEDLENMY 240
Dy 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFPNPSQEDLENMY 240

Qy 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSC TPNYSVNI REELKLANVVFPRCLLVQ 300
Dy 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSC TPNYSVNI REELKLANVVFPRCLLVQ 300

Qy 301 RCGNCGCGTVNWRSC TNSGKT VKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Dy 301 RCGNCGCGTVNWRSC TNSGKT VKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

Qy 361 DCICSSRPPR 370
Dy 361 DCICSSRPPR 370

RESULT 7
AAG65601
ID AAG65601 standard; protein; 370 AA.
XX
AC AAG65601;
XX
DT 07-JAN-2002 (first entry)
XX
DE Human zveg4 polypeptide.
XX
KW Zveg4; bone; ligament; cartilage; osteoblast; osteoclast; chondrocyte;
KW bone cancer; osteonclerosis; bone defect; osteogenesis; osteoporosis;
KW osteopathic; vulnerary; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT Protein /note= "secretory peptide"
FT Protein 19..370
FT Protein /note= "mature protein"
FT Domain 52..179
FT Domain /note= "CUB domain"
FT Region 180..257
FT Domain /note= "propeptide-like sequence"
FT Domain 258..370
FT Domain /note= "growth factor domain"
XX

PN WO200157083-A1.
XX
PD 09-AUG-2001.
XX
FF 03-MAY-2000; 2000WO-US012095.
XX
FF 04-FEB-2000; 2000US-0180169P.
PR 31-MAR-2000; 2000US-00540224.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gilbertson DG, Hart CE;
PI WPI: 2001-611088/70.
XX N-PSDB; AAH47772.
XX
PT Use of zveg4 polypeptide for promoting bone, ligament or cartilage
PT growth in mammal at site of fracture, implant, and bone graft, and for
PT promoting growth or differentiation of osteoblasts, chondrocytes in
PT culture.
XX
XX Example 2; Page 44-47; 57pp; English.
XX
CC The invention relates to the use of zveg4 polypeptide for promoting
CC bone, ligament or cartilage growth in a mammal, and for promoting
CC proliferation or differentiation of osteoblasts, osteoclasts,
CC chondrocytes or bone marrow stem cells in culture. For promoting
CC cartilage growth, chondrocytes are cultured ex vivo in presence of the
CC zveg4 polypeptide and then placed into mammal where cartilage is to be
CC grown. Zveg4 polypeptide is useful for promoting growth of bone,
CC ligament or cartilage in a mammal at a site of bony defect such as
CC fracture, bone graft, implant or periodontal pocket, in humans and non-
CC human animals such as domestic animals including livestock and companion
CC animals. Zveg4 is used for promoting growth of bone, ligament, or
CC cartilage in conditions of bone defects following therapeutic treatments
CC of bone cancers or other conditions characterized by increased bone loss
CC or decreased bone formation, or elevation of peak bone mass in pre-
CC menopausal woman. It is also useful for healing bone following radiation
CC -induced osteonclerosis, repairing bone defects arising from surgery, and
CC promotion of bone healing in plastic surgery, increasing bone formation
CC during distraction osteogenesis, treating bone injuries including repair
CC of cartilage and ligament and treatment of osteoporosis. The present
CC sequence represents a human zveg4 polypeptide
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLI FVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRRDET IQVG 60
Dy 1 MHRLI FVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRRDET IQVG 60

Qy 61 NGYVQSRPFNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLAEAEENDICRYDFVEVEDIS 120
Dy 61 NGYVQSRPFNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLAEAEENDICRYDFVEVEDIS 120

Qy 121 ETSIIIRGWCCHKEVPPRIKSRTNQIKITPKSDDYFVAKGPKFIYYSLLLEDFOFAAASE 180
Dy 121 ETSIIIRGWCCHKEVPPRIKSRTNQIKITPKSDDYFVAKGPKFIYYSLLLEDFOFAAASE 180

Qy 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFPNPSQEDLENMY 240
Dy 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFPNPSQEDLENMY 240

Qy 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSC TPNYSVNI REELKLANVVFPRCLLVQ 300
Dy 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSC TPNYSVNI REELKLANVVFPRCLLVQ 300

Qy 301 RCGNCGCGTVNWRSC TNSGKT VKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Dy 301 RCGNCGCGTVNWRSC TNSGKT VKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 8
AAE00999
ID AAE00999 standard; protein; 370 AA.
XX
AC AAE00999;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human Zvegfg4 protein which forms heteromultimer with Zvegfg3 protein.
XX
KW Human; Zvegfg3 antagonist; cell proliferation; stellate cell activation;
KW extracellular matrix production; fibrosis; VEGF-R; PDGF-C;
KW platelet-derived growth factor; PDGF; vascular endothelial growth factor;
KW VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;
KW chronic active hepatitis; fulminant viral hepatitis; amyloidosis;
KW diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;
KW asbestosis; renal arteriosclerosis; post necrotic cirrhosis;
KW diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis;
KW pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;
KW bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;
KW fibroproliferative disorder; Zvegfg4 protein.
XX
OS Homo sapiens.
XX
PN WO200128586-A1.
XX
PD 26-APR-2001.
XX
PF 23-OCT-2000; 2000WO-US029270.
XX
PR 21-OCT-1999; 99US-0161653P.
PR 12-NOV-1999; 99US-0165255P.
PR 01-AUG-2000; 2000US-022223P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gilbertson DG;
XX
XX WPI; 2001-300278/31.
DR
XX
XX Use of zvegfg3 antagonist for reducing fibroproliferative disorder of
PT kidney, liver and bone, reducing extracellular matrix production,
PT treating fibrosis or reducing stellate cell activation in mammal.
XX
PS Disclosure; Page 62-63; 70pp; English.
XX
CC The patent discloses materials and methods for reducing cell
CC proliferation or extracellular matrix production, treating fibrosis and
CC reducing stellate cell activation in a mammal. The method comprises
CC administering a composition containing a Zvegfg3 antagonist in combination
CC with a delivery vehicle. The Zvegfg3 is a protein that is structurally
CC related to platelet-derived growth factor (PDGF) and the vascular
CC endothelial growth factors (VEGF). The Zvegfg3 protein is also designated
CC as "VEGF-R" and "PDGF-C". The Zvegfg3 antagonist is useful to block the
CC mitogenic effects of zvegfg3 and thereby to inhibit or prevent and treat
CC keloids, scleroderma, fibrotic disorders of liver such as chronic active
CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and alpha-1
CC -antitrypsin deficiency, fibrotic disorders of the kidney such as
CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders
CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,
CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,
CC fibrotic disorders of pancreas, fibroproliferative disorders of the
CC vasculature such as transplant vasculopathy and fibroproliferative
CC disorders of the bone such as osteopetrosis and hyperostosis. The present
CC sequence is human Zvegfg4 protein which forms a heteromultimer with Zvegfg3
CC protein

XX Sequence 370 AA;
SQ
Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLTDLYRRDETQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLTDLYRRDETQVKG 60
QY 61 NGYVQSPRPNSYPNLLLTWELHSEENTRIQLVFDNQFGLBEAENDICRYDFEVEDIS 120
Db 61 NGYVQSPRPNSYPNLLLTWELHSEENTRIQLVFDNQFGLBEAENDICRYDFEVEDIS 120
QY 121 ETSITIRGWCQKHEVPPRIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLLEDFQPAASE 180
Db 121 ETSITIRGWCQKHEVPPRIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLLEDFQPAASE 180
QY 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPSWOEDLENNY 240
Db 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPSWOEDLENNY 240
QY 241 LDTPRYGRSYHDKRSKVDLDRLNDDAKRYSCPTPNYSVNIIEELKLANVVFPPCLLVQ 300
Db 241 LDTPRYGRSYHDKRSKVDLDRLNDDAKRYSCPTPNYSVNIIEELKLANVVFPPCLLVQ 300
QY 301 RCGNGCGCTVNRSCCTNSGKTVKKYHEVLQFEGHKKRRGRAKTMALVDIQLDHHRC 360
Db 301 RCGNGCGCTVNRSCCTNSGKTVKKYHEVLQFEGHKKRRGRAKTMALVDIQLDHHRC 360
QY 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 9
AAB85529
ID AAB85529 standard; protein; 370 AA.
XX
AC AAB85529;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human secreted protein (clone Id HGCNC48).
XX
KW Secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide; human;
KW ophthalmological; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200155430-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001431.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 12-SEP-2000; 2000US-0231968P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Komatsuulis CA, Baker KP, Birse CE, Soppet DR;
PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;
PI Fiscella M, Ni J, Ruben SM, Barash SC;
XX
DR WPI; 2001-476220/51.
DR N-PSDB; AAH46939.
XX
PT 17 isolated nucleic acid molecules encoding human secreted proteins, used

to preventing, treating or ameliorating a medical condition.

Claim 11; Page 447-449; 482pp; English.

The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can also be used in diagnosing a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angioneurosis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a human secreted protein

Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRILFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLLDLYRDETQVKG 60
DB 1 MHRILFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLLDLYRDETQVKG 60

QY 61 NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
DB 61 NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120

QY 121 ETSTIIRGRWCCHKVEPPRIKSRNTQIKITPKSDDYFVAKGPKIYYSLLEDQFQAAASE 180
DB 121 ETSTIIRGRWCCHKVEPPRIKSRNTQIKITPKSDDYFVAKGPKIYYSLLEDQFQAAASE 180

QY 181 TNWESVTSISGVSNSPSVTDPTLIADALDKKTAETFDVEDLLKYNPESQWEDLENNY 240
DB 181 TNWESVTSISGVSNSPSVTDPTLIADALDKKTAETFDVEDLLKYNPESQWEDLENNY 240

QY 241 LDTPRYGRSYHDKRSKVDLRDLNDDAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQ 300
DB 241 LDTPRYGRSYHDKRSKVDLRDLNDDAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQ 300

QY 301 RCGNCGCGTVNRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERC 360
DB 301 RCGNCGCGTVNRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERC 360

QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 10
AAE15819 standard; protein; 370 AA.

XX AAE15819;
AC AAE15819;
XX XX
DT 26-MAR-2002 (first entry)
XX Human LP85 protein #1.
XX LP85; platelet-derived growth factor; PDGF; antiinflammatory; vulneryary;
KW osteopathic; neuroprotective; tranquilliser; musculoskeletal disorder;
KW

KW MSD; therapy; bone growth; cartilage differentiation; wound healing;
KW neuron growth; bone fracture; osteoporosis; osteopenia; arthritis;
KW sarcopenia; periodontal disease; tissue atrophy; endocrine disorder;
KW muscle loss; immobility; bone density.

XX Homo sapiens.

XX Location/Qualifiers
FH Key 1..12
FH Peptide /label= Signal_peptide
FT Protein 13..370
FT /label= Human_mature_LP85_protein
XX
PN WO200189450-A2.
XX
XX 29-NOV-2001.
XX
XX 08-MAY-2001; 2001WO-US011755.
XX
XX 19-MAY-2000; 2000US-0205424P.
PR 11-JAN-2001; 2001US-0261071P.
PR 11-JAN-2001; 2001US-0261076P.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Beals JM, Gonzalez-Dewhitt PA, Hammond LJ, Lu J, Na S, Su EW;
PI Witcher DR, Wroblewski VJ;
XX
XX WPI; 2002-083040/11.
DR N-PSDB; AAD15819.
XX
XX Analog of a platelet-derived growth factor homolog, LP85 useful for
PT treating osteoporosis, arthritis, sarcopenia, wounds, has one or more
PT amino acid substitutions which destroy the tripeptidyl sequence of native
PT LP85.
XX
XX Claim 11; Page 109-110; 117pp; English.

The present invention relates to LP85, an analogue of platelet-derived growth factor (PDGF) homologue. Sequences of the invention are useful for the manufacture of a medicament for treating musculoskeletal disorder (MSD) which include promoting bone growth, cartilage differentiation and function, wound healing, neuron growth, preventing cartilage degradation or neuronal degeneration. They are useful for treating bone fractures, osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease, tissue atrophy, traumatised connective tissues, grafted connective tissue and/or transplanted organs, bone or muscle loss due to malignancy, endocrine disorders and immobility. They are also used for prophylactically increasing or maintaining bone density in a mammal. The present sequence is human LP85 protein

Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRILFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLLDLYRDETQVKG 60
DB 1 MHRILFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLLDLYRDETQVKG 60

QY 61 NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
DB 61 NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120

QY 121 ETSTIIRGRWCCHKVEPPRIKSRNTQIKITPKSDDYFVAKGPKIYYSLLEDQFQAAASE 180
DB 121 ETSTIIRGRWCCHKVEPPRIKSRNTQIKITPKSDDYFVAKGPKIYYSLLEDQFQAAASE 180

QY 181 TNWESVTSISGVSNSPSVTDPTLIADALDKKTAETFDVEDLLKYNPESQWEDLENNY 240
DB 181 TNWESVTSISGVSNSPSVTDPTLIADALDKKTAETFDVEDLLKYNPESQWEDLENNY 240

CC osteoclasts, chondrocytes or bone marrow stem cells, where the bone
 CC marrow stem cells are harvested from a patient prior to culture. The
 CC method is therefore useful for treating osteoporosis
 XX
 XX
 SQ Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 5; Length 370;
 Best Local Similarity 100.0%; Pred. No. 1e-188;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLRYRDETIQVKG 60
 DB 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLRYRDETIQVKG 60

QY 61 NGYVQSPFPNSYPNRLLLTWRLHSEENTRIQLVFDNQFGLSEAEANDICRYDFVEVEDIS 120
 DB 61 NGYVQSPFPNSYPNRLLLTWRLHSEENTRIQLVFDNQFGLSEAEANDICRYDFVEVEDIS 120

QY 121 ETSTIIRGRWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
 DB 121 ETSTIIRGRWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180

QY 181 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFDTVEDLLKYFNPSHQEDLENNY 240
 DB 181 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFDTVEDLLKYFNPSHQEDLENNY 240

QY 241 LDPYRGRSYHDKRSKVDLRLNDADAKRYSCPTPRNYSVNIREEKLKLANVFFPRCLLVQ 300
 DB 241 LDPYRGRSYHDKRSKVDLRLNDADAKRYSCPTPRNYSVNIREEKLKLANVFFPRCLLVQ 300

QY 301 RCGNGCGCTVNRSTCNSGKTVKYYHEVLFQEPGHIKRRGRAKTMALVDIQLDHHERC 360
 DB 301 RCGNGCGCTVNRSTCNSGKTVKYYHEVLFQEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY 361 DCICSSRRPR 370
 DB 361 DCICSSRRPR 370

RESULT 14
 ABB79588
 ID ABB79588 standard; protein; 370 AA.
 XX
 AC ABB79588;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human zvegfg protein.
 XX
 KW Zvegfg; human; kidney; acute tubular necrosis; nephrotropic;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= Signal_peptide
 FT Protein 19..370
 FT /label= CUB domain+interdomain+growth_factor domain
 FT /note= "alternatively comprises residues 24-370, 25-370,
 FT 35-370 or 52-370"
 FT Domain 180..370
 FT /label= Growth_factor domain
 FT /label= 246..370
 FT /label= Growth_factor domain
 FT /note= "alternatively comprises residues 250-370 or 258-
 FT 370"
 XX
 PN WO200260467-A2.
 PD 08-AUG-2002.
 XX
 PD 26-OCT-2001; 2001WO-US050155.
 PF

XX 30-OCT-2000; 2000US-0244479P.
 PR (ZYMO) ZYMOGENETICS INC.
 XX
 PA Hart CE, Topouzis S;
 XX
 PI WPI; 2002-590847/63.
 XX N-PSDB; ABN84420.
 DR
 XX Improving kidney function, or enhancing proliferation or survival of
 PT kidney tubule epithelial cells or epithelial cell precursors in a mammal
 PT comprises administering a zvegfg protein or zvegfg protein-encoding
 PT polynucleotide.
 XX
 PS Claim 4; Page 38-39; 45pp; English.
 XX
 CC The present sequence is the protein sequence of human vegf4, a protein
 CC which activates the alpha-alpha, alpha-beta and beta-beta forms of the
 CC platelet-derived growth factor (PDGF) receptor. Zvegfg is structurally
 CC related to PDGF and vascular endothelial growth factor. Structural
 CC predictions suggest the polypeptide can form homomultimers or
 CC heteromultimers that act on tissues by modulating cell proliferation,
 CC migration, differentiation or metabolism. The polypeptide comprises a
 CC growth factor domain having a cysteine knot structure, and a CUB domain. A
 CC propeptide-like sequence extends from residue 180 to either residue 245,
 CC 249 or 257. Zvegfg can thus be prepared in a variety of multimeric forms
 CC including zvegfg4(19-370), zvegfg4(52-370), zvegfg4(246-370), zvegfg4(250-
 CC 370) and zvegfg4(258-370). Expression of zvegfg4 polynucleotide in cultured
 CC mammalian cells results in production of a disulfide-bonded, dimeric
 CC protein. Mitogenically active protein is generated upon proteolytic
 CC processing to remove the CUB and interdomain regions. An active growth
 CC factor domain dimer can be produced directly by expressing a truncated
 CC polynucleotide. A claimed method of improving kidney function, or
 CC enhancing proliferation or survival of kidney tubule epithelial cells or
 CC epithelial cell precursors in a mammal, comprises administering a
 CC composition containing a zvegfg4 protein or zvegfg4 protein-encoding
 CC polynucleotide in combination with a delivery vehicle. The method is
 CC especially useful for improving kidney function in a mammal suffering
 CC from acute tubular necrosis. The zvegfg4 protein is preferably a disulfide
 CC -bonded dimer of 2 polypeptide chains comprising residues 258-370, 250-
 CC 370 or 246-370 of the present sequence, or a disulfide-bonded dimer of 2
 CC polypeptide chains, each chain consisting of residues x - y, where the
 CC protein is optionally glycosylated, and x is 16, 17, 18, 19, 20, 21, 22,
 CC 24, 25, 35, 52, 175, 177, 178, 179, 180, 181, 182, 183, 184, 185,
 CC 246, 250, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262 or 263, and y
 CC is 365, 366, 367, 369 or 370
 XX
 SQ Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 5; Length 370;
 Best Local Similarity 100.0%; Pred. No. 1e-188;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLRYRDETIQVKG 60
 DB 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLRYRDETIQVKG 60

QY 61 NGYVQSPFPNSYPNRLLLTWRLHSEENTRIQLVFDNQFGLSEAEANDICRYDFVEVEDIS 120
 DB 61 NGYVQSPFPNSYPNRLLLTWRLHSEENTRIQLVFDNQFGLSEAEANDICRYDFVEVEDIS 120

QY 121 ETSTIIRGRWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
 DB 121 ETSTIIRGRWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180

QY 181 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFDTVEDLLKYFNPSHQEDLENNY 240
 DB 181 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFDTVEDLLKYFNPSHQEDLENNY 240

QY 241 LDPYRGRSYHDKRSKVDLRLNDADAKRYSCPTPRNYSVNIREEKLKLANVFFPRCLLVQ 300
 DB 241 LDPYRGRSYHDKRSKVDLRLNDADAKRYSCPTPRNYSVNIREEKLKLANVFFPRCLLVQ 300

```
QY 301 RCGNCGCGTVMWRSCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMALVDIQLDHHERC 360
    |||
Db 301 RCGNCGCGTVMWRSCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMALVDIQLDHHERC 360
    |||
QY 361 DCICSSRPPR 370
    |||
Db 361 DCICSSRPPR 370
    |||

RESULT 15
ABG78502
ID ABG78502 standard; protein; 370 AA.
XX
AC ABG78502;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human FCTR 1 protein.
XX
KW 30664188 antigen; blood; cancer; human; FCTR.
XX
OS Homo sapiens.
XX
PN WO200259618-A2.
XX
PD 01-AUG-2002.
XX
PF 16-NOV-2001; 2001WO-US048901.
XX
PR 16-NOV-2000; 2000US-00715332.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
PI Jeffers M, Andrews D, Larochele W;
DR
DR WPI: 2002-619187/66.
DR N-PSDB; ABS63515.
XX
Detecting presence or amount of 30664188 antigen in a sample, by
PT contacting the biological sample with agent that binds the antigen, and
PT detecting the presence or amount of agent bound to the antigen.
XX
Example 1; Page 11-13; 177pp; English.
XX
The present invention relates to a new method of detecting the presence
CC of 30664188 antigen in a sample. The invention is useful for detecting
CC the presence of 30664188 in a biological sample (e.g. blood or its
CC component originating from a mammal, preferably human), and for
CC contributing to diagnosis of cancer in a subject. The present amino acid
CC sequence represents a human FCTR protein, as described in the methods of
CC the invention
XX
Sequence 370 AA;
Query Match 100.0%; Score 1994; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNNHLDLYRRDETIOVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNNHLDLYRRDETIOVKG 60
QY 61 NGYVQSPFPNPNYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPFPNPNYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS 120
QY 121 ETSIIIRGCGHKHEVPRIKSRNQIKITPKSDDYFVAKPGFKIYSLLEDFOFAASE 180
Db 121 ETSIIIRGCGHKHEVPRIKSRNQIKITPKSDDYFVAKPGFKIYSLLEDFOFAASE 180
QY 181 TNWESVTSSISGVSNPSVDPTLIADALDKKIAEFTVDDLKLYFNPESWQEDLENNY 240
```

```
Db 181 TNWESVTSSISGVSNPSVDPTLIADALDKKIAEFTVDDLKLYFNPESWQEDLENNY 240
    |||
QY 241 LDTPRYGRSYHDKRSKVDLRLNDDAKRYSCPTPNYSVNIREBLKLANVVFFPRCLLVQ 300
    |||
Db 241 LDTPRYGRSYHDKRSKVDLRLNDDAKRYSCPTPNYSVNIREBLKLANVVFFPRCLLVQ 300
    |||
QY 301 RCGNCGCGTVMWRSCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMALVDIQLDHHERC 360
    |||
Db 301 RCGNCGCGTVMWRSCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMALVDIQLDHHERC 360
    |||
QY 361 DCICSSRPPR 370
    |||
Db 361 DCICSSRPPR 370
    |||

RESULT 16
ABG76575
ID ABG76575 standard; protein; 370 AA.
XX
AC ABG76575;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human secreted protein #7.
XX
KW Human; secreted protein; autoimmune disease; blood coagulation disorder;
KW blood platelet disorder; hyperproliferative disorder; renal disorder;
KW neurodegenerative disorder; cardiovascular disorder; vascular disorder;
KW respiratory disorder; endocrine disorder; reproductive disorder;
KW gastrointestinal disorder; infectious disease; antianaemic; cytostatic;
KW antiarthritic; immunosuppressive; antiaesthmic; antidiabetic;
KW antiinflammatory; antipsoriatic; antiparkinsonian; neuroprotective.
XX
OS Homo sapiens.
XX
PN US2002120103-A1.
XX
PD 29-AUG-2002.
XX
27-JUL-2001; 2001US-00915582.
31-JAN-2000; 2000US-0179065P.
04-FEB-2000; 2000US-0180628P.
12-SEP-2000; 2000US-0231968P.
17-JAN-2001; 2001WO-US001431.
(ROSE/) ROSEN C A.
PA (KOMA/) KOMATSOUKIS G A.
PA (BAKE/) BAKER K P.
PA (BIRS/) BIRSE C E.
PA (SOPP/) SOPPET D R.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIP/) WEI P.
PA (EBNE/) EBNER R.
PA (DUAN/) DUAN D R.
PA (SHIY/) SHI Y.
PA (CHOI/) CHOI G H.
PA (FISC/) FISCELLA M.
PA (NIJJ/) NI J.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;
PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;
PI Fiscella M, Ni J, Ruben SM, Barash SC;
XX
WPI: 2002-609160/65.
DR N-PSDB; ABS58475.
XX
New secreted polypeptides and encoding polynucleotides, useful for
PT preventing, treating and diagnosing diseases e.g. anemia, cancer,
```

PT diabetes, asthma, psoriasis, Parkinson's and Alzheimer's.
PS Claim 11; Page 389-390; 238pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule which encodes
CC a human secreted protein. The sequences are useful for diagnosing or
CC diagnosing a susceptibility to a pathological condition in a subject
CC comprising determining the presence or absence of a mutation in the DNA
CC or expression of the protein. The sequences are useful for identifying a
CC binding partner to the protein comprising contacting the protein with a
CC binding partner and determining whether the binding partner effects an
CC activity. The DNA and protein sequences are used for preventing, treating
CC or ameliorating a medical condition such as an autoimmune disease (e.g.
CC multiple sclerosis, myasthenia gravis), blood coagulation disorders (e.g.
CC afibrinogenemia, haemophilia), blood platelet disorders (e.g.
CC thrombocytopenia), hyperproliferative disorders (e.g. sarcoidosis, Sezary
CC syndrome), neurodegenerative disorders (e.g. Alzheimer's disease,
CC Parkinson's disease), renal disorders (e.g. renal vein thrombosis, kidney
CC infarction), cardiovascular disorders (e.g. cardiac arrest,
CC pericarditis), vascular disorders (e.g. aneurysm, ischaemia), respiratory
CC disorders (e.g. tonsillitis, laryngitis), endocrine disorders (e.g.
CC acromegaly, thyrotoxicosis), reproductive disorders (gonorrhea,
CC anorchia), gastrointestinal disorders (e.g. gastroenteritis, pyloric
CC stenosis), infectious diseases (e.g. polio, rubella) and cancer. The
CC Sequences ABG76569-ABG76616 represent human secreted proteins of the
CC invention
XX
XX Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTLYRDETTLQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTLYRDETTLQVKG 60
QY 61 NGVQSPRPNSYPNLLTLTWLHQSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
Db 61 NGVQSPRPNSYPNLLTLTWLHQSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
QY 121 ETSTIIRGRCGHEKVPVPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLLEDFQPAASE 180
Db 121 ETSTIIRGRCGHEKVPVPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLLEDFQPAASE 180
QY 181 TWVESVTSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
Db 181 TWVESVTSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
QY 241 LOTPRYGRSYHDKRSKVDLDRNLDDAKRYSCYCTPRNYSVNIREEELKLANVVFPPRCLLVQ 300
Db 241 LOTPRYGRSYHDKRSKVDLDRNLDDAKRYSCYCTPRNYSVNIREEELKLANVVFPPRCLLVQ 300
QY 301 RCGNGCGCTVNWRSCTNSGKTVKKYHYEVLQPEPGHIKRRGRAKTMALVDIOLDHHERC 360
Db 301 RCGNGCGCTVNWRSCTNSGKTVKKYHYEVLQPEPGHIKRRGRAKTMALVDIOLDHHERC 360
QY 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 17
ABG64733
ID ABG64733 standard; protein; 370 AA.
XX
XX
XX ABG64733;
AC
DT 27-AUG-2002 (First entry)
XX
XX Human albumin fusion protein #1408.
DE
XX
XX Albumin fusion protein; therapeutic protein X; human albumin; HA;

KW human serum albumin; HSA; cancer; reproductive disorder;
KW digestive disorder; immune disorder; endocrine disorder;
KW haematopoietic disorder; neural disorder; connective disorder;
KW cytostatic; antifertility; antiinflammatory; antitumor;
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neurologic;
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
osteopathic; antiarthritic.
XX
OS Homo sapiens.
XX
XX Synthetic.
PN WO200177137-A1.
XX
XX 18-OCT-2001.
PD
PF 12-APR-2001; 2001WO-US011988.
XX
PR 12-APR-2000; 2000US-0229358P.
PR 25-APR-2000; 2000US-0199384P.
PR 21-DEC-2000; 2000US-0256931P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Haeeltine WA;
PI
XX
XX WPI; 2002-010886/01.
XX
XX New fusion protein for treating disease e.g. diabetes comprises an
PT albumin fused to a therapeutic protein.
XX
XX Claim 1; Page 1459-1460; 2102pp; English.
XX
CC The present invention relates to albumin fusion proteins comprising a
CC therapeutic protein X and human albumin (HA, also known as human serum
CC albumin, HSA). The proteins are useful for treating a disease or disorder
CC that may be modulated by therapeutic protein X. The albumin extends the
CC shelf-life of protein X, and may increase its biological in vitro/in vivo
CC activity. The protein is useful for treating and diagnosing disorders
CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
CC disease, ulcerative colitis), immune disorders (e.g. acquired
CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX
XX Sequence 370 AA;
SQ
Query Match 100.0%; Score 1994; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTLYRDETTLQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTLYRDETTLQVKG 60
QY 61 NGVQSPRPNSYPNLLTLTWLHQSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
Db 61 NGVQSPRPNSYPNLLTLTWLHQSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
QY 121 ETSTIIRGRCGHEKVPVPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLLEDFQPAASE 180
Db 121 ETSTIIRGRCGHEKVPVPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLLEDFQPAASE 180
QY 181 TWVESVTSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
Db 181 TWVESVTSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
QY 241 LOTPRYGRSYHDKRSKVDLDRNLDDAKRYSCYCTPRNYSVNIREEELKLANVVFPPRCLLVQ 300
Db 241 LOTPRYGRSYHDKRSKVDLDRNLDDAKRYSCYCTPRNYSVNIREEELKLANVVFPPRCLLVQ 300
QY 301 RCGNGCGCTVNWRSCTNSGKTVKKYHYEVLQPEPGHIKRRGRAKTMALVDIOLDHHERC 360

Db 301 RCGNCGCGTVNWRSCCTNSGKTVKYEVLQFEPGHIKRGRAKTMALVDIQLDHHERC 360
 QY 361 DCICSSRRPPR 370
 Db 361 DCICSSRRPPR 370

RESULT 18

ABP51640
 ID ABP51640 standard; protein; 370 AA.

XX AC ABP51640;

XX DT 30-SEP-2002 (first entry)

XX DE Human zvegfg4 protein SEQ ID NO:2.

XX KW Human; zvegfg4; cell proliferation; extracellular matrix production;
 KW fibroproliferative disorder; PDGF-D; platelet derived growth factor;
 KW PDGF; vascular endothelial growth factor; VEGF; cytosatic; nephrotropic;
 KW hepatotropic; antiinflammatory; osteopatic; antiarthritic; metastasis;
 KW prostate tumour; prostate cancer; glomerulonephritis; lupus nephritis;
 KW diabetic glomerulosclerosis; renal arteriosclerosis; nephrotic syndrome;
 KW chronic active hepatitis; cirrhosis; osteopetrosis; osteosclerosis;
 KW hyperostosis; osteoarthritis.

XX OS Homo sapiens.

XX PN US2002064832-A1.

XX PD 30-MAY-2002.

XX PF 14-MAR-2001; 2001US-00808972.

XX PR 03-MAY-1999; 99US-0132250P.

XX PR 10-NOV-1999; 99US-0164463P.

XX PR 04-FEB-2000; 2000US-0180169P.

XX PR 03-MAY-2000; 2000US-0056459S.

XX PR 26-SEP-2000; 2000US-0235293P.

XX PA (HART/) HART C E.

XX PA (TOPO/) TOPOUZIS S.

XX PA (GILB/) GILBERTSON D G.

XX PI Hart CE, Topouzis S, Gilbertson DG;

XX PS WPI; 2002-573696/61.

XX PS N-PSDB; ABQ73239.

XX PT Reducing proliferation or extracellular matrix production by a cell in a

XX PT mammal, useful for treating fibroproliferative disorders of bone, liver

XX PT and kidney, comprises administering a zvegfg4 antagonist.

XX PS Example 3; Page 19-20; 34pp; English.

XX CC The present invention describes a method for reducing proliferation of or
 CC extracellular matrix production by a cell in a mammal. The method
 CC comprises administering to the mammal a composition comprising a
 CC therapeutically effective amount of a zvegfg4 antagonist chosen from anti-
 CC zvegfg4 antibodies, inhibitory polynucleotides, inhibitors of zvegfg4
 CC activation, and mitogenically inactive, receptor-binding variants of
 CC zvegfg4. Zvegfg4 (also called PDGF-D) is a multi-domain protein that is
 CC structurally related to platelet derived growth factor (PDGF) and
 CC vascular endothelial growth factors (VEGF). Zvegfg4 has cytosatic,
 CC nephrotropic, hepatotropic, antiinflammatory, osteopatic and
 CC antiarthritic activities. The method is useful for reducing proliferation
 CC of mesangial, epithelial, endothelial, smooth muscle, fibroblast,
 CC osteoblast, osteoclast, neuronal, stromal, stellate or interstitial cells
 CC in a mammal, in particular proliferation of prostate tumour cells, and
 CC for reducing extracellular matrix production by a cell in a mammal
 CC suffering from a fibroproliferative disorder of kidney, bone or liver. In
 CC particular it is useful for reducing stellate cell activation. The method

CC is useful for reducing metastasis of prostate cancer cells to bone in a
 CC mammal and for treating a fibroproliferative disorder of kidney, liver or
 CC bone in a mammal. Fibroproliferative disorders of the kidney include,
 CC glomerulonephritis, diabetic glomerulosclerosis, lupus nephritis, renal
 CC arteriosclerosis and nephrotic syndrome, disorders of the liver include
 CC chronic active hepatitis and many other types of cirrhosis, and disorders
 CC of the bone include osteopetrosis, hyperostosis, osteosclerosis,
 CC osteoarthritis, and ectopic bone formation in metastatic prostate cancer.
 CC The present sequence represents human zvegfg4, which is used in an example
 CC from the present invention

XX SQ Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 5; Length 370;
 Best Local Similarity 100.0%; Pred. No. 1a-188;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRILFVYTLICANFCSCRDTSATPQASIKALRNANLRDSENHITDLYRRDETIOVKG 60

Db 1 MHRILFVYTLICANFCSCRDTSATPQASIKALRNANLRDSENHITDLYRRDETIOVKG 60

QY 61 NGYVQSPRPNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLERAENDICRYDFVEVEDIS 120

Db 61 NGYVQSPRPNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLERAENDICRYDFVEVEDIS 120

QY 121 ETSTIIIRGWCCHKKEVPRIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOPAASE 180

Db 121 ETSTIIIRGWCCHKKEVPRIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOPAASE 180

QY 181 TNWESVTSSISGVSNSPSVTDPTLIADALDKIAEFTVEDLLKYFNPSQWEDLENNY 240

Db 181 TNWESVTSSISGVSNSPSVTDPTLIADALDKIAEFTVEDLLKYFNPSQWEDLENNY 240

QY 241 LDTPRYGRSYHDKRSKVDLDRLNDDAKRYSCCTPRNSYVNIREBKLANVYVFFRCLLVQ 300

Db 241 LDTPRYGRSYHDKRSKVDLDRLNDDAKRYSCCTPRNSYVNIREBKLANVYVFFRCLLVQ 300

QY 301 RCGNCGCGTVNWRSCCTNSGKTVKYEVLQFEPGHIKRGRAKTMALVDIQLDHHERC 360

Db 301 RCGNCGCGTVNWRSCCTNSGKTVKYEVLQFEPGHIKRGRAKTMALVDIQLDHHERC 360

QY 361 DCICSSRRPPR 370

Db 361 DCICSSRRPPR 370

RESULT 19

ABU72430

ID ABU72430 standard; protein; 370 AA.

XX AC ABU72430;

XX DT 17-JUN-2003 (first entry)

XX DE Human growth factor homologue ZVEGFA.

XX KW Human; growth factor homologue; ZVEGFA; proliferation; differentiation;
 KW migration; mesenchymal cell; cell surface semaphorin; neuropilin;
 KW neurite growth; cardiovascular development; limb development;
 KW cartilage development; T-cell; B-cell; rheumatoid arthritis; cancer;
 KW autoimmune disease; inflammation; retinopathy; haemangioma;
 KW ischaemic event; neuropathy; acute nerve damage; stroke;
 KW central nervous system disease; peripheral nervous system disease;
 KW chromosome 11q22.3-23.1.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 52..370 /note= "Specifically claimed in claim 7"

XX FT Region 52..253 /note= "Specifically claimed in claim 7"

XX FT Region 180..370

FT /note= "Specifically claimed in claim 5"
 FT 250. .370
 FT /note= "Specifically claimed in claim 7"
 FT 250. .370
 FT /note= "Specifically claimed in claim 2"
 FT 258. .370
 FT /note= "Specifically claimed in claim 1"
 XX
 PN US6495668.B1.
 XX
 PD 17-DEC-2002.
 XX
 PD 03-MAY-2000; 2000US-00564595.
 XX
 PD 03-MAY-1999; 99US-0132250P.
 PR 10-NOV-1999; 99US-0164463P.
 PR 04-FEB-2000; 2000US-0180169P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
 XX
 DR WPI: 2003-352153/33.
 DR N-PSDB; AC64109.
 XX
 XX Isolated growth factor analogue ZVEGF4 proteins for pharmaceutical
 PT composition as, e.g. therapeutic agents, diagnostic agents, and research
 PT tools and reagents, includes polypeptides from amino acid residues.
 PT
 XX
 PS Claim 1; Col 71-72; 67pp; English.
 XX
 CC The invention relates to an isolated protein comprising a first
 CC polypeptide disulphide-bonded to a second polypeptide. The first and
 CC second polypeptides are from 113-138 amino acid residues and comprises
 CC 258-370 amino acid residues of human growth factor homologue ZVEGF4. The
 CC protein stimulates proliferation, differentiation, or migration of
 CC mesenchymal cells and may modulate activities mediated by cell surface
 CC semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-
 CC semaphorin interactions which may be of use in neurite growth,
 CC cardiovascular development, cartilage and limb development, T- and B-cell
 CC functions as well as treating rheumatoid arthritis, various forms of
 CC cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas,
 CC ischaemic events, neuropathies, acute nerve damage, central nervous
 CC system diseases and peripheral nervous system diseases including stroke.
 CC The isolated protein is also used for a pharmaceutical composition as
 CC therapeutic agents, diagnostic agents, and research tools and reagents.
 CC It can be used in the study and regulation of cell and tissue
 CC development, as components of cell culture media. The proteins can form
 CC homomultimers or heteromultimers that act on tissues to control organ
 CC development by modulating cell proliferation, migration, differentiation,
 CC or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3
 CC -23.1. The present sequence represents human ZVEGF4
 XX
 SQ Sequence 370 AA;
 Query Match 100.0%; Score 1994; DB 6; Length 370;
 Best Local Similarity 100.0%; Pred. No. 1e-188;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRLIFVYTLICANFCSRDTSATPOSASIKALRNANLRDSESNHLTDLYRDETIQVG 60
 DB 1 MRLIFVYTLICANFCSRDTSATPOSASIKALRNANLRDSESNHLTDLYRDETIQVG 60
 QY 61 NGYVQSPRPNSYPNRLTLTLRLHSENTRIQLVFDNQFGLSEAEINDICRYDFVEVEDIS 120
 DB 61 NGYVQSPRPNSYPNRLTLTLRLHSENTRIQLVFDNQFGLSEAEINDICRYDFVEVEDIS 120
 QY 121 ETSITIRGWCHEKVPPIKRTNQIKITFKSDDYFVAKPGFKIYYSLEDFQPAASE 180
 DB 121 ETSITIRGWCHEKVPPIKRTNQIKITFKSDDYFVAKPGFKIYYSLEDFQPAASE 180
 QY 181 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFTVDLLKYNFNPESWQEDLENMY 240
 DB 181 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFTVDLLKYNFNPESWQEDLENMY 240

Db 181 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFTVDLLKYNFNPESWQEDLENMY 240
 QY 241 LDTPRYGRGSYHDKRSKVDLRLNDDAKRYSCCTPRNYSVNIREEELKLANVFFPRLCLVQ 300
 Db 241 LDTPRYGRGSYHDKRSKVDLRLNDDAKRYSCCTPRNYSVNIREEELKLANVFFPRLCLVQ 300
 QY 301 RCGNCGCGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIOLDHHERC 360
 Db 301 RCGNCGCGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIOLDHHERC 360
 QY 361 DCICSSRRPR 370
 Db 361 DCICSSRRPR 370
 RESULT 20
 ABG76397
 ID ABG76397 standard; protein; 370 AA.
 XX
 AC ABG76397;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 DE Human growth factor homologue, zvegfg4.
 XX
 KW Human; growth factor homologue; zvegfg4; fibroblast; smooth muscle cell;
 KW cell-surface platelet-derived growth factor alpha receptor; PDGF;
 KW full-thickness skin wound; female reproductive tract; duodenal ulcer;
 KW prolonged bleeding; periodontal disease; tissue adhesive; liver damage;
 KW revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis;
 KW chronic active hepatitis; hepatic chronic passive congestion; stroke;
 KW central haemorrhagic necrosis; hepatic vein thrombosis; ischaemia;
 KW portal vein thrombosis; cardiac sclerosis; new vessel formation;
 KW endothelial precursor stem cell; neovascularisation; wound healing;
 KW organ transplant; tissue grafting; peripheral neuropathy; spinal cord;
 KW sensory neurite outgrowth; brain disease; head injury; paralysis;
 KW spinal injury; neurodegenerative disease; diabetic retinopathy;
 KW psoriasis; arthritis; scleroderma; keloid; liver fibrosis; psoriasis;
 KW lung fibrosis; kidney fibrosis; glomerulosclerosis; cancer;
 KW proliferative vascular disorder; ocular neovascularisation;
 KW inflammatory disorder; rheumatoid arthritis; vasculogenesis;
 KW angiogenesis; nervous system disorder; cystostatic; hepatotropic;
 KW vulnery; tranquiliser; cerebroprotective; neuroprotective; nootropic;
 KW ophthalmological; dermatological; coagulant; cardiant.
 XX
 OS Homo sapiens.
 PN US2002177193-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 02-MAY-2002; 2002US-00139583.
 XX
 PR 07-DEC-1998; 98US-0111173P.
 PR 06-JUL-1999; 99US-0142576P.
 PR 21-OCT-1999; 99US-0161653P.
 PR 12-NOV-1999; 99US-0165255P.
 PR 07-DEC-1999; 99US-00457066.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
 PI Gilbertson DG, West JW;
 PI
 XX WPI: 2003-328485/31.
 DR N-PSDB; ABX93177.
 XX
 XX New isolated zvegfg3 polypeptide, useful for treating cancer, Alzheimer's
 PT disease, Parkinson's disease, chronic active hepatitis, hepatic vein
 PT thrombosis, comprises growth factor domain and CUB domain.
 XX
 XX Disclosure; Page 51-52; 73pp; English.

CC The present invention relates to the isolation of a growth factor
CC homologue referred to as zvegfg3, and the polynucleotide sequence encoding
CC it. The zvegfg3 polypeptide is useful for stimulating the growth of
CC fibroblasts or smooth muscle cells, or for activating a cell-surface
CC platelet-derived growth factor (PDGF) alpha receptor. The zvegfg3
CC polypeptide is useful as a PDGF alpha receptor agonist and thus is useful
CC for treating full-thickness skin wounds, female reproductive tract and
CC prolonged bleeding, periodontal disease, damaged liver tissue, and
CC duodenal ulcers. The polypeptide is also useful as an additive in tissue
CC adhesives for promoting revascularisation of healing tissue. The zvegfg3
CC polypeptide is also useful for treating liver damage including damage due
CC to liver disease, chronic active hepatitis, hepatic chronic passive
CC congestion (CPC), central haemorrhagic necrosis (CHN), hepatic vein
CC thrombosis, portal vein thrombosis, cardiac sclerosis, and many types of
CC cirrhosis. The polypeptide is useful for enhancing expansion and
CC mobilisation of endothelial precursor stem cells, creating and
CC stabilising new vessel formation in areas requiring neovascularisation,
CC including areas of ischaemia, organ transplants, wound healing, and
CC tissue grafting. It may be used for treating peripheral neuropathies by
CC increasing spinal cord and sensory neurite outgrowth, and as part of
CC therapeutic treatment for the regeneration of neurite outgrowths
CC following strokes, brain damage caused by head injuries, and paralysis
CC caused by spinal injuries. Application may also be made in treating
CC neurodegenerative diseases (e.g. multiple sclerosis, Alzheimer's disease,
CC Parkinson's disease), diabetic retinopathy, psoriasis, arthritis,
CC scleroderma, and reducing fibrosis, keloids, liver fibrosis, lung
CC fibrosis, kidney fibrosis, and glomerulosclerosis. An antibody that binds
CC zvegfg3 is useful for blocking the mitogenic, chemotactic, or angiogenic
CC effects of zvegfg3, and for treating proliferative vascular disorders,
CC ocular neovascularisation, inflammatory disorders, rheumatoid arthritis,
CC psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis,
CC and diseases of the nervous system. The present sequence represents human
CC zvegfg4
XX

SQ Sequence 370 AA;

Query Match	100.0%;	Score 1994;	DB 6;	Length 370;
Best Local Similarity	100.0%;	Pred. No. 1e-188;		
Matches 370;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLTDLYRRDETIQVKG	60	
Db	1	MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLTDLYRRDETIQVKG	60	
Qy	61	NGYVQSPRPNSYPENLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVEDIS	120	
Db	61	NGYVQSPRPNSYPENLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVEDIS	120	
Qy	121	ETSTIIRGWCHEVPVPRIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLEDQFPAASE	180	
Db	121	ETSTIIRGWCHEVPVPRIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLEDQFPAASE	180	
Qy	181	TNWSVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSQWQEDLENMY	240	
Db	181	TNWSVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSQWQEDLENMY	240	
Qy	241	LDTPRYGRSVHDKSKVDLRLNDADKYSCTPRNYSVINREELKLANVVFPRCLLVQ	300	
Db	241	LDTPRYGRSVHDKSKVDLRLNDADKYSCTPRNYSVINREELKLANVVFPRCLLVQ	300	
Qy	301	RCGNCGGCTVNRSCCTCNCKTKVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC	360	
Db	301	RCGNCGGCTVNRSCCTCNCKTKVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC	360	
Qy	361	DCICSSRPDR 370		
Db	361	DCICSSRPDR 370		

Search completed: November 10, 2005, 09:31:31
Job time : 183.723 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:24:47 ; Search time 45.9627 Seconds
(without alignments)
600.925 Million cell updates/sec

Title: US-10-606-055-2

Perfect score: 1994

Sequence: 1 MRLIFVYLTICANFCSCRD.....DIQLDHERDCICSSRPPR 370

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*

2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*

3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*

4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/PTUS-COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1994	100.0	370	4	US-09-457-066-37
2	1994	100.0	370	4	US-09-540-224-2
3	1994	100.0	370	4	US-09-564-595D-2
4	1994	100.0	370	4	US-09-706-968-37
5	1994	100.0	370	4	US-09-808-972-2
6	1994	100.0	370	4	US-09-823-033-5
7	1994	100.0	370	4	US-09-438-046-8
8	1994	100.0	370	4	US-10-139-583-37
9	1994	100.0	370	4	US-10-039-847A-2
10	1742	87.4	322	4	US-09-438-046-6
11	1737	87.1	370	4	US-09-540-224-4
12	1737	87.1	370	4	US-09-564-595D-53
13	1737	87.1	370	4	US-09-808-972-4
14	1737	87.1	370	4	US-10-039-847A-4
15	1403	70.4	317	4	US-09-564-595D-56
16	1357.5	68.1	316	4	US-09-564-595D-55
17	1095	54.9	303	4	US-09-564-595D-57
18	1061.5	53.2	302	4	US-09-564-595D-54
19	982	49.2	300	4	US-09-438-046-4
20	752	37.7	345	4	US-09-457-066-43
21	752	37.7	345	4	US-09-564-595D-35
22	752	37.7	345	4	US-09-706-968-43
23	752	37.7	345	4	US-09-823-033-4
24	752	37.7	345	4	US-10-139-583-43
25	744	37.3	374	4	US-09-468-647A-118
26	742.5	37.2	345	3	US-09-040-220D-2
27	742.5	37.2	345	4	US-09-457-066-2

28	742.5	37.2	345	4	US-09-265-686-2	Sequence 2, Appli
29	742.5	37.2	345	4	US-09-540-224-5	Sequence 5, Appli
30	742.5	37.2	345	4	US-09-564-595D-33	Sequence 33, Appli
31	742.5	37.2	345	4	US-09-706-968-2	Sequence 2, Appli
32	742.5	37.2	345	4	US-09-723-749-2	Sequence 2, Appli
33	742.5	37.2	345	4	US-09-823-033-2	Sequence 2, Appli
34	742.5	37.2	345	4	US-09-468-647A-101	Sequence 101, App
35	742.5	37.2	345	4	US-09-468-647A-110	Sequence 110, App
36	742.5	37.2	345	4	US-09-468-647A-130	Sequence 130, App
37	742.5	37.2	345	4	US-10-139-583-2	Sequence 2, Appli
38	741	37.2	354	4	US-09-468-647A-120	Sequence 120, App
39	741	37.2	355	4	US-09-468-647A-122	Sequence 122, App
40	739.5	37.1	323	4	US-09-468-647A-1	Sequence 1, Appli
41	739.5	37.1	345	4	US-09-468-647A-2	Sequence 2, Appli
42	739.5	37.1	345	4	US-09-468-647A-103	Sequence 103, App
43	651	32.6	121	4	US-09-438-046-18	Sequence 18, Appli
44	637	31.9	119	4	US-09-438-046-19	Sequence 19, Appli
45	490	24.6	282	4	US-09-468-647A-112	Sequence 112, App
46	380	19.1	66	4	US-09-438-046-2	Sequence 2, Appli
47	330	16.5	168	4	US-09-468-647A-27	Sequence 27, Appli
48	330	16.5	168	4	US-09-468-647A-126	Sequence 126, App
49	329.5	16.5	132	4	US-09-468-647A-29	Sequence 29, Appli
50	328.5	16.5	149	4	US-09-468-647A-124	Sequence 124, App
51	308.5	15.5	113	4	US-09-468-647A-99	Sequence 99, Appli
52	306	15.3	167	4	US-09-468-647A-111	Sequence 111, App
53	295.5	14.8	111	4	US-09-468-647A-26	Sequence 26, Appli
54	292	14.6	227	4	US-09-468-647A-114	Sequence 114, App
55	292	14.6	227	4	US-09-468-647A-116	Sequence 116, App
56	187.5	9.4	439	4	US-09-949-016-9260	Sequence 9260, Ap
57	187.5	9.4	788	1	US-08-572-223-1	Sequence 1, Appli
58	187.5	9.4	986	4	US-09-285-385C-19	Sequence 19, Appli
59	187.5	9.4	986	4	US-09-949-016-6690	Sequence 6690, Ap
60	186.5	9.4	730	3	US-08-872-757-2	Sequence 2, Appli
61	186.5	9.4	730	3	US-09-850-048A-2	Sequence 2, Appli
62	186.5	9.4	1015	4	US-09-285-385C-2	Sequence 2, Appli
63	183.5	9.2	1012	4	US-09-285-385C-4	Sequence 4, Appli
64	180.5	9.1	101	3	US-09-374-133-6	Sequence 6, Appli
65	177.5	8.9	113	4	US-09-438-046-22	Sequence 22, Appli
66	176	8.8	923	4	US-09-583-638-2	Sequence 2, Appli
67	174.5	8.8	923	4	US-09-439-711C-2	Sequence 2, Appli
68	174.5	8.8	986	3	US-08-872-757-4	Sequence 4, Appli
69	174.5	8.8	986	4	US-09-850-048A-4	Sequence 4, Appli
70	172.5	8.7	591	3	US-08-991-408-4	Sequence 4, Appli
71	172.5	8.7	591	3	US-09-432-473-4	Sequence 4, Appli
72	172.5	8.7	1013	2	US-08-866-650-5	Sequence 5, Appli
73	172.5	8.7	1013	2	US-09-021-287-5	Sequence 5, Appli
74	172.5	8.7	1013	3	US-08-991-408-2	Sequence 2, Appli
75	172.5	8.7	1013	3	US-09-240-473-5	Sequence 5, Appli
76	172.5	8.7	1013	3	US-09-432-473-2	Sequence 2, Appli
77	172.5	8.7	1013	4	US-09-285-385C-20	Sequence 20, Appli
78	171	8.6	3623	4	US-09-341-461-2	Sequence 2, Appli
79	169.5	8.5	110	4	US-09-341-461-29	Sequence 29, Appli
80	167.5	8.4	103	3	US-09-374-135-5	Sequence 5, Appli
81	167.5	8.4	112	4	US-09-438-046-21	Sequence 21, Appli
82	167	8.4	922	4	US-09-439-711C-4	Sequence 4, Appli
83	167	8.4	922	4	US-09-116-473-4	Sequence 4, Appli
84	166.5	8.4	1013	2	US-08-866-650-3	Sequence 3, Appli
85	166.5	8.4	1013	2	US-09-021-287-3	Sequence 3, Appli
86	166.5	8.4	1013	3	US-09-240-473-3	Sequence 3, Appli
87	164	8.2	923	3	US-08-936-135-6	Sequence 6, Appli
88	164	8.2	923	3	US-09-439-711C-6	Sequence 6, Appli
89	159	8.0	909	3	US-08-936-135-18	Sequence 18, Appli
90	159	8.0	909	4	US-09-439-711C-18	Sequence 18, Appli
91	159	8.0	926	3	US-08-936-135-20	Sequence 20, Appli
92	159	8.0	926	4	US-09-439-711C-20	Sequence 20, Appli
93	159	8.0	931	4	US-09-583-638-4	Sequence 4, Appli
94	158.5	7.9	111	4	US-09-341-461-30	Sequence 30, Appli
95	157	7.9	113	4	US-09-438-046-23	Sequence 23, Appli
96	157	7.9	901	3	US-08-936-135-22	Sequence 22, Appli
97	157	7.9	901	4	US-09-439-711C-22	Sequence 22, Appli
98	157	7.9	906	3	US-08-936-135-24	Sequence 24, Appli
99	157	7.9	906	4	US-09-439-711C-24	Sequence 24, Appli
100	157	7.9	909	3	US-08-936-135-8	Sequence 8, Appli

d

ALIGNMENTS

RESULT 1

US-09-457-066-37
; Sequence 37, Application US/09457066
; Patent No. 6432673

GENERAL INFORMATION:

; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.

; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3

; FILE REFERENCE: 98-60

; CURRENT APPLICATION NUMBER: US/09/457,066

; CURRENT FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 37

; LENGTH: 370

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-457-066-37

Query Match 100.0%; Score 1994; DB 4; Length 370;

Best Local Similarity 100.0%; Pred. No. 1.2e-197;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MHRLIFVYTLICANFCSCRDTSATPQASIKALRNANLRDESNHLLTDLRRDETQVKG	60
Db	1	MHRLIFVYTLICANFCSCRDTSATPQASIKALRNANLRDESNHLLTDLRRDETQVKG	60
Qy	61	NGYVQSPRFNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS	120
Db	61	NGYVQSPRFNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS	120
Qy	121	ETSTIIRGWCHEKVPRIKSRNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE	180
Db	121	ETSTIIRGWCHEKVPRIKSRNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE	180
Qy	181	TNWSVTSSISGVSNPSVTDPTLIADALDKKIAEFTVDELLKYFNPSQWEDLENNY	240
Db	181	TNWSVTSSISGVSNPSVTDPTLIADALDKKIAEFTVDELLKYFNPSQWEDLENNY	240
Qy	241	LDTPRYGRSVHDKRSKVDLRLNDADAKRYCTPRNSVNIREEELKLANVVFPPRCLLVQ	300
Db	241	LDTPRYGRSVHDKRSKVDLRLNDADAKRYCTPRNSVNIREEELKLANVVFPPRCLLVQ	300
Qy	301	RCGNGCGGTNNRSCCTNSGKTVKHYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC	360
Db	301	RCGNGCGGTNNRSCCTNSGKTVKHYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC	360
Qy	361	DCICSSRRPPR 370	
Db	361	DCICSSRRPPR 370	

RESULT 2

US-09-540-224-2

; Sequence 2, Application US/09540224

; Patent No. 6468543

GENERAL INFORMATION:

; APPLICANT: Gilbertson, Debra G.

; APPLICANT: Hart, Charles E.

; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,

; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4

; FILE REFERENCE: 00-28

; CURRENT APPLICATION NUMBER: US/09/540,224

; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-2

Query Match 100.0%; Score 1994; DB 4; Length 370;

Best Local Similarity 100.0%; Pred. No. 1.2e-197;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MHRLIFVYTLICANFCSCRDTSATPQASIKALRNANLRDESNHLLTDLRRDETQVKG	60
Db	1	MHRLIFVYTLICANFCSCRDTSATPQASIKALRNANLRDESNHLLTDLRRDETQVKG	60
Qy	61	NGYVQSPRFNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS	120
Db	61	NGYVQSPRFNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS	120
Qy	121	ETSTIIRGWCHEKVPRIKSRNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE	180
Db	121	ETSTIIRGWCHEKVPRIKSRNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE	180
Qy	181	TNWSVTSSISGVSNPSVTDPTLIADALDKKIAEFTVDELLKYFNPSQWEDLENNY	240
Db	181	TNWSVTSSISGVSNPSVTDPTLIADALDKKIAEFTVDELLKYFNPSQWEDLENNY	240
Qy	241	LDTPRYGRSVHDKRSKVDLRLNDADAKRYCTPRNSVNIREEELKLANVVFPPRCLLVQ	300
Db	241	LDTPRYGRSVHDKRSKVDLRLNDADAKRYCTPRNSVNIREEELKLANVVFPPRCLLVQ	300
Qy	301	RCGNGCGGTNNRSCCTNSGKTVKHYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC	360
Db	301	RCGNGCGGTNNRSCCTNSGKTVKHYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC	360
Qy	361	DCICSSRRPPR 370	
Db	361	DCICSSRRPPR 370	

RESULT 3

US-09-564-595D-2

; Sequence 2, Application US/09564595D

; Patent No. 6495668

GENERAL INFORMATION:

; APPLICANT: Gilbert, Teresa

; APPLICANT: Hart, Charles E.

; APPLICANT: Sheppard, Paul O.

; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4

; FILE REFERENCE: 99-19

; CURRENT APPLICATION NUMBER: US/09/564,595D

; CURRENT FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: US 09/304,216

; PRIOR FILING DATE: 1999-05-03

; PRIOR APPLICATION NUMBER: US 60/164,463

; PRIOR FILING DATE: 1999-11-10

; PRIOR APPLICATION NUMBER: US 60/180,169

; PRIOR FILING DATE: 2000-02-04

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 370

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-564-595D-2

Query Match 100.0%; Score 1994; DB 4; Length 370;


Best Local Similarity 100.0%; Pred. No. 1.2e-197;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MHR	LIFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLTDLYRDETIOVKG	60
Dd	1	MHR	LIFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLTDLYRDETIOVKG	60
Qy	61	NGY	VQSPRFPNYSYPRNLLTWRLHSOENRIQLVFEDNQFGLBEAENDICRYDFVEVEDIS	120
Dd	61	NGY	VQSPRFPNYSYPRNLLTWRLHSOENRIQLVFEDNQFGLBEAENDICRYDFVEVEDIS	120
Qy	121	ETS	TIIIRGRWCCHKVEVPRIKSRNTNQIKITPKSDDYFVAKPFGFKIYYSLLEDFQPAAASE	180
Dd	121	ETS	TIIIRGRWCCHKVEVPRIKSRNTNQIKITPKSDDYFVAKPFGFKIYYSLLEDFQPAAASE	180
Qy	181	TNES	VTSSISGVSYNSPSVTDPTLIIADLDKKIAEFTDVEDLLKYFPESWQEDLENNY	240
Dd	181	TNES	VTSSISGVSYNSPSVTDPTLIIADLDKKIAEFTDVEDLLKYFPESWQEDLENNY	240
Qy	241	LDT	PRTYGRSVHDKRSKVDLORLNDDAKRYCTPPNYSVNIREELKIANVFFPRCLLVQ	300
Dd	241	LDT	PRTYGRSVHDKRSKVDLORLNDDAKRYCTPPNYSVNIREELKIANVFFPRCLLVQ	300
Qy	301	RCGN	C CGGTWNWSCTCNSGKT VKKYHEVLQFEPGHIKRGRAKTMALVDIQLDHHERC	360
Dd	301	RCGN	C CGGTWNWSCTCNSGKT VKKYHEVLQFEPGHIKRGRAKTMALVDIQLDHHERC	360
Qy	361	DCI	CSSRRPR 370	
Dd	361	DCI	CSSRRPR 370	

	Query Match	100.0%;	Score 1994;	DB 4;	Length 370;
	Best Local Similarity	100.0%;	Pred. No. 1.2e-197;		
	Matches 370;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MHRLIIFYVTLICANFCSCROTSATPQASIKALRNANLRDSEHNHLLTLYRRDETIOVKG	60		
Db	1	MHRLIIFYVTLICANFCSCROTSATPQASIKALRNANLRDSEHNHLLTLYRRDETIOVKG	60		
Qy	61	NGYVQSPRFNSYPRNLLLTWRLHQSQENTRIQLVFDNQFGLGEEAENDICRYDFVEVEDIS	120		
Db	61	NGYVQSPRFNSYPRNLLLTWRLHQSQENTRIQLVFDNQFGLGEEAENDICRYDFVEVEDIS	120		
Qy	121	ETSTIIRGRWCGHKHEVPRIKSRPNQKITFKSDDDYFVAKPGFKIYVSLLEDFQPAASE	180		
Db	121	ETSTIIRGRWCGHKHEVPRIKSRPNQKITFKSDDDYFVAKPGFKIYVSLLEDFQPAASE	180		
Qy	181	TNWEVSTSSISGVSYNSPVSVDPTPLIADALDKKIAEFDTVEDLLKYNFNSGWSQEDLNMY	240		

Db	181	TNWSVTSISSGVNSPVSVDPTLIADALDKKIAEFTVEDLLKYFNPESWQEDLENNY	240
Qy	241	LDTPRYGRSVYHDRKSKVDLORLNDADAKRYSCTPRNSVNIREEUKLANVVFPRCLLVQ	300
Db	241	LDTPRYGRSVYHDRKSKVDLORLNDADAKRYSCTPRNSVNIREEUKLANVVFPRCLLVQ	300
Qy	301	RCGNCGCGTWNWRSCTCNSOKTVKKYHEVLQFEPGHIKRRGRAKTMAVDIQLDHHERC	360
Db	301	RCGNCGCGTWNWRSCTCNSOKTVKKYHEVLQFEPGHIKRRGRAKTMAVDIQLDHHERC	360
Qy	361	DCICSSRPPR 370	
Db	361	DCICSSRPPR 370	



```

RESULT 5
US-09-808-972-2
; Sequence 2, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPLASIA
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-972-2

```

Query Match	100.0%;	Score 1994;	DB 4;	Length 370;
Best Local Similarity	100.0%;	Pred. No. 1.2e-197;		
Matches 370;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MHRLIFVYTLICANFCS	CRDTSATPQSGASIIKALNANLRR	DESNNHLDLYRRDETIVQVG 60
Db	1	MHRLIFVYTLICANFCS	CRDTSATPQSGASIKALNANLRR	DESNNHLDLYRRDETIVQVG 60
Qy	61	NGYVQSRPFNSYPRNLL	TLWRHLSQENTRQLVPDNO	FGLEEAEANDICRYDFVEVEDIS 120
Db	61	NGYVQSRPFNSYPRNLL	TLWRHLSQENTRQLVPDNO	FGLEEAEANDICRYDFVEVEDIS 120
Qy	121	ETSTPIIRGWC	GHKEVPRIKSR	TNOIKITPKSDDYFVAKGFKIYSLLEDFOPAAMASE 180
Db	121	ETSTPIIRGWC	GHKEVPRIKSR	TNOIKITPKSDDYFVAKGFKIYSLLEDFOPAAMASE 180
Qy	181	TNNEVSTSSISGV	SNPSVTDPLIADALOKIAE	FDTVEDLLKYFNPESQWEDLENNY 240
Db	181	TNNEVSTSSISGV	SNPSVTDPLIADALOKIAE	FDTVEDLLKYFNPESQWEDLENNY 240
Qy	241	LDPTRYGRSVYH	DRKSKVDLR	LNDNDAKRYSCTPRNYSVNIREEUKLANVVFPPRCLLVQ 300
Db	241	LDPTRYGRSVYH	DRKSKVDLR	LNDNDAKRYSCTPRNYSVNIREEUKLANVVFPPRCLLVQ 300
Qy	301	RCGCNCGCGT	WNRSCTCNSGKTVKKY	HEVLQFEPGHIKRRGRAKTMALVDIQLDHERC 360

Db 301 RCGNCGCGTVNWRSCNCGTKVKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
| | | | |
Db 361 DCICSSRPPR 370

RESULT 6

US-09-823-033-5
; Sequence 5, Application US/09823033
; Patent No. 6663870
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-5

Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRILFVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRDETIQVKG 60
| | | | |
Db 1 MHRILFVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRDETIQVKG 60
Qy 61 NGYVQSPRPFPNSYPNRLLLTWRLHSQENTRIQLVFDNQFGLSEAENDICRYDFVEVEDIS 120
| | | | |
Db 61 NGYVQSPRPFPNSYPNRLLLTWRLHSQENTRIQLVFDNQFGLSEAENDICRYDFVEVEDIS 120
Qy 121 ETSTIIRGRWCGHKVEPPRIKSRNTQIKITPKSDDYFVAKPGFKIYYSLLED FQPAASE 180
| | | | |
Db 121 ETSTIIRGRWCGHKVEPPRIKSRNTQIKITPKSDDYFVAKPGFKIYYSLLED FQPAASE 180
Qy 181 TNWESVTSISGVSNPSVTDPTLIADALDKKTAEDFTVEDLLKYNPESQEDLENNY 240
| | | | |
Db 181 TNWESVTSISGVSNPSVTDPTLIADALDKKTAEDFTVEDLLKYNPESQEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCTPRNYSVNI REELKLANVVFPPRCLLVQ 300
| | | | |
Db 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCTPRNYSVNI REELKLANVVFPPRCLLVQ 300
Qy 301 RCGNCGCGTVNWRSCNCGTKVKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
| | | | |
Db 301 RCGNCGCGTVNWRSCNCGTKVKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
| | | | |
Db 361 DCICSSRPPR 370

RESULT 7

US-09-438-046-8
; Sequence 8, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: AEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik

; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-8

Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRILFVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRDETIQVKG 60
| | | | |
Db 1 MHRILFVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRDETIQVKG 60
Qy 61 NGYVQSPRPFPNSYPNRLLLTWRLHSQENTRIQLVFDNQFGLSEAENDICRYDFVEVEDIS 120
| | | | |
Db 61 NGYVQSPRPFPNSYPNRLLLTWRLHSQENTRIQLVFDNQFGLSEAENDICRYDFVEVEDIS 120
Qy 121 ETSTIIRGRWCGHKVEPPRIKSRNTQIKITPKSDDYFVAKPGFKIYYSLLED FQPAASE 180
| | | | |
Db 121 ETSTIIRGRWCGHKVEPPRIKSRNTQIKITPKSDDYFVAKPGFKIYYSLLED FQPAASE 180
Qy 181 TNWESVTSISGVSNPSVTDPTLIADALDKKTAEDFTVEDLLKYNPESQEDLENNY 240
| | | | |
Db 181 TNWESVTSISGVSNPSVTDPTLIADALDKKTAEDFTVEDLLKYNPESQEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCTPRNYSVNI REELKLANVVFPPRCLLVQ 300
| | | | |
Db 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCTPRNYSVNI REELKLANVVFPPRCLLVQ 300
Qy 301 RCGNCGCGTVNWRSCNCGTKVKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
| | | | |
Db 301 RCGNCGCGTVNWRSCNCGTKVKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
| | | | |
Db 361 DCICSSRPPR 370

RESULT 8

US-10-139-583-37
; Sequence 37, Application US/10139583
; Patent No. 6814965
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVBEF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066

```
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-139-583-37

Query Match      100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60

QY 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120

QY 121 ETSTIIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSTIIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180

QY 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESQEDLENNY 240
Db 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESQEDLENNY 240

QY 241 LDTPRYGRSHYDRSKVDLDRNDADAKRYCTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Db 241 LDTPRYGRSHYDRSKVDLDRNDADAKRYCTPRNYSVNIREEKLANVVFPPRCLLVQ 300

QY 301 RCGNGCGCTVNRWRSCTNSGKTVKXYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNGCGCTVNRWRSCTNSGKTVKXYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 9
US-10-039-847A-2
; Sequence 2, Application US/10039847A
; Patent No. 6827938
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; TITLE OF INVENTION: KIDNEY FUNCTION
; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039,847A
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-039-847A-2

Query Match      100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60

QY 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120

QY 121 ETSTIIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSTIIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180

QY 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESQEDLENNY 240
Db 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESQEDLENNY 240

QY 241 LDTPRYGRSHYDRSKVDLDRNDADAKRYCTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Db 241 LDTPRYGRSHYDRSKVDLDRNDADAKRYCTPRNYSVNIREEKLANVVFPPRCLLVQ 300

QY 301 RCGNGCGCTVNRWRSCTNSGKTVKXYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNGCGCTVNRWRSCTNSGKTVKXYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 10
US-09-438-046-6
; Sequence 6, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTIN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OBSTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D,
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 322
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-438-046-6

Query Match      87.4%; Score 1742; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.2e-171;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 LYRDETQVKGNGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDI 108
Db 1 LYRDETQVKGNGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDI 60

QY 109 CRYDFVEVEDISETSTIIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYS 168
Db 61 CRYDFVEVEDISETSTIIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYS 120

QY 169 LLEDQPAASSETNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 228
```

```
Db 121 LLEDFQPAASSETNWESVTSISGVSYNSPVSVDPTLIADALDKKIAEFDVEDLLKYFN 180
Qy 229 PESQOEDLENNYLDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCVTPRNSVNIREEELKJA 288
Db 181 PESQOEDLENNYLDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCVTPRNSVNIREEELKJA 240
Qy 289 NVVFPFRCLLVORCGNCGCTVNWRSCTCHSGKTVKKYHEVLQFEPGHIKRRGAKTMA 348
Db 241 NVVFPFRCLLVORCGNCGCTVNWRSCTCHSGKTVKKYHEVLQFEPGHIKRRGAKTMA 300
Qy 349 LVDIQLDHHERCDCICSSRPPR 370
Db 301 LVDIQLDHHERCDCICSSRPPR 322
```

RESULT 11

```
US-09-540-224-4
; Sequence 4, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; PRIOR FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-540-224-4
```

```
Query Match 87.1%; Score 1737; DB 4; Length 370;
Best Local Similarity 85.1%; Pred. No. 4.8e-171;
Matches 315; Conservative 25; Mismatches 30; Indels 0; Gaps 0;
```

```
Qy 1 MHLRFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNNHLDLYRRDETIOVKG 60
Db 1 MQLVLVLSILLCANFSCVDPDTFATFORASIKALRNANLRDESNNHLDLYQREENIQVTS 60
Qy 61 NGYVQSPRFPNSYPNLLLTWLRHSQENTRIQLVFDNQFGLAEAEENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRFPNSYPNLLLTWLRHSQENTRIQLSFDHQFGLAEAEENDICRYDFVEVEEVS 120
Qy 121 ETSTIIRGWCCHKEVPPRIKSRITNOIKITPKSDDYFVAKPGFKIYYSLLEDQFPAASE 180
Db 121 ESSIVRGRWCCHKEIPRITSRTNOIKITPKSDDYFVAKPGFKIYYSFVEDQFPAASE 180
Qy 181 TNWESVTSISGVSYNSPVSVDPTLIADALDKKIAEFDVEDLLKYFNPEQOEDLENNY 240
Db 181 TNWESVTSISGVSYNSPVSVDPTLIADALDKTVAEFTVEDLLKHFNPVSWQDDLENLY 240
Qy 241 LDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCVTPRNSVNIREEELKLANVVFPPRCLLVQ 300
Db 241 LDTPHYGRSYHDKRSKVDLDRNLDDAKRYSCVTPRNSVNIREEELKLTNAVFFPRCLLVQ 300
Qy 301 RCGNCGCTVNWRSCTCHSGKTVKKYHEVLQFEPGHIKRRGAKTMAVLDIQLDHHERC 360
Db 301 RCGNCGCTVNWRSCTCHSGKTVKKYHEVLKFEFGHFKRRGAKAKNMALVLDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370
```

RESULT 12

```
US-09-564-595D-53
```

```
; Sequence 53, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-564-595D-53
```

```
Query Match 87.1%; Score 1737; DB 4; Length 370;
Best Local Similarity 85.1%; Pred. No. 4.8e-171;
Matches 315; Conservative 25; Mismatches 30; Indels 0; Gaps 0;
```

```
Qy 1 MHLRFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNNHLDLYRRDETIOVKG 60
Db 1 MQLVLVLSILLCANFSCVDPDTFATFORASIKALRNANLRDESNNHLDLYQREENIQVTS 60
Qy 61 NGYVQSPRFPNSYPNLLLTWLRHSQENTRIQLVFDNQFGLAEAEENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRFPNSYPNLLLTWLRHSQENTRIQLSFDHQFGLAEAEENDICRYDFVEVEEVS 120
Qy 121 ETSTIIRGWCCHKEVPPRIKSRITNOIKITPKSDDYFVAKPGFKIYYSLLEDQFPAASE 180
Db 121 ESSIVRGRWCCHKEIPRITSRTNOIKITPKSDDYFVAKPGFKIYYSFVEDQFPAASE 180
Qy 181 TNWESVTSISGVSYNSPVSVDPTLIADALDKKIAEFDVEDLLKYFNPEQOEDLENNY 240
Db 181 TNWESVTSISGVSYNSPVSVDPTLIADALDKTVAEFTVEDLLKHFNPVSWQDDLENLY 240
Qy 241 LDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCVTPRNSVNIREEELKLANVVFPPRCLLVQ 300
Db 241 LDTPHYGRSYHDKRSKVDLDRNLDDAKRYSCVTPRNSVNIREEELKLTNAVFFPRCLLVQ 300
Qy 301 RCGNCGCTVNWRSCTCHSGKTVKKYHEVLQFEPGHIKRRGAKTMAVLDIQLDHHERC 360
Db 301 RCGNCGCTVNWRSCTCHSGKTVKKYHEVLKFEFGHFKRRGAKAKNMALVLDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370
```

RESULT 13

```
US-09-808-972-4
; Sequence 4, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
```



```

; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-808-972-4

Query Match      87.1%; Score 1737; DB 4; Length 370;
Best Local Similarity 85.1%; Pred. No. 4,8e-171;
Matches 315; Conservative 25; Mismatches 30; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRRDESNNHLLTDLYRDETIQVKG 60
Db 1 MORLVLSILLCANFSCYPDTFATPORASIKALRNANLRRDESNNHLLTDLYQREENIQVTS 60
QY 61 NGVQSPRPNSYPNLLLTWLRHSEKTRIQLSFDHQFGLBEAENDICRYDFVEVEVDS 120
Db 61 NGHVQSPRPNSYPNLLLTWLRHSEKTRIQLSFDHQFGLBEAENDICRYDFVEVEVDS 120
QY 121 ETSITIRGRCWCGHKEVPPRIKSRITNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ESSTVVRGRCWCGHKEIPRIITSRITNQIKITFKSDDYFVAKPGFKIYYSFVDFQPEASE 180
QY 181 TNWESVTSISGVSYNSPSVTDPTLIADALOKKIAEFDTVEDLLKYNFNPESQOEDLENNY 240
Db 181 TNWESVTSISGVSYNSPSVTDPTLIADALOKKIAEFDTVEDLLKYNFNPESQOEDLENNY 240
QY 241 LDTPHYRGSRVHDKRSKVDLDRNDKAKRYSCYCTPNYSVNIREEELKLANVFFPRCLLVQ 300
Db 241 LDTPHYRGSRVHDKRSKVDLDRNDKAKRYSCYCTPNYSVNIREEELKLANVFFPRCLLVQ 300
QY 301 RCGNCGCGTVNWRSCNCGKTVKKYHEVLQFEPGHIKRRGRKAKTMALVDIQLDHHERC 360
Db 301 RCGNCGCGTVNWRSCNCGKTVKKYHEVLQFEPGHIKRRGRKAKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 15
US-09-564-595D-56
; Sequence 56, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: Sheppard, Paul O.
; FILE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-56

Query Match      70.4%; Score 1403; DB 4; Length 317;
Best Local Similarity 83.8%; Pred. No. 1,4e-136;
Matches 263; Conservative 14; Mismatches 33; Indels 4; Gaps 2;

QY 52 RDETIQVKGNGYVQSPRPNSYPNLLLTWLRHSEKTRIQLSFDHQFGLBEAENDICRY 111
Db 1 RDETIQVKGNGYVQSPRPNSYPNLLLTWLRHSEKTRIQLSFDHQFGLBEAENDICRY 60
QY 112 DFVEVEDISESTIIRGRCWCGHKEVPPRIKSRITNQIKITFKSDDYFVAKPGFKIYYSLL 171
Db 61 DFVEVEDISESTIIRGRCWCGHKEVPPRIKSRITNQIKITFKSDDYFVAKPGFKIYYSLL 120
QY 172 DFQPAASETNWESVTSISGVSYNSPSVTDPTLIADALOKKIAEFDTVEDLLKYNFNPES 231
Db 121 DFQPAASETNWESVTSISGVSYNSPSVTDPTLIADALOKKIAEFDTVEDLLKYNFNPES 180
```

Qy 232 WOEDLENNYLDTPRYGRSYHDKSK-VLDRLNDDAKRYSCCTPRNYSVNIREEKLANV 290
Db 181 WOEDLENNYLDTPRYGRSYHDKSKVVDLLNLTTEEVRLYSCTPRNFSVIREELKRTD 240
Qy 291 VFFRCLLVQRCGGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALV 350
Db 241 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP---KTGVRGLHLSLT 297
Qy 351 DIQLDHHERCDCIC 364
Db 298 DVALEHHEECDCVC 311

RESULT 16

US-09-564-595D-55
; Sequence 55, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55

Query Match 68.1%; Score 1357.5; DB 4; Length 316;
Best Local Similarity 80.0%; Pred. No. 7.3e-132;
Matches 256; Conservative 24; Mismatches 33; Indels 7; Gaps 4;

Qy 53 DETIQVKGNGYVQSPRPNSYPNLLLTWRLHS-QENTRIQLVFDNQFGLBEAENDICRY 111
Db 2 ERIITVSTNGSIHSPRPHTYPRNTLVMLVAVEENWVIQLTFDERPGLDEPDDICKY 61
Qy 112 DFVEVEDISETSTIIRGWCCHKEVPPRIKSRTNQIKITPKSDDYFVAKPGFKIYSL-L 170
Db 62 DFVEVEEPSDGT--ILGRWCOSGTVPGRQISGKNQIRIRFVSDBEYFFPSEPGFCIHYNIVM 119
Qy 171 EDFQPAASATNWSVTSSISGVSYNSPSVTDPTLIADALDKIAEFTVDDLKYFNPE 230
Db 120 PQFTEA---EINWSVTSSISGVSYNSPSVTDPTLIADALDKIAEFTVDDLKYFNPE 176
Qy 231 SQWEDLENNYLDTPRYGRSYHDKSKVDLRLNDDAKRYSCCTPRNYSVNIREEKLANV 290
Db 177 SQWEDLENNYLDTPRYGRSYHDKSKVDLRLNDDAKRYSCCTPRNYSVNIREEKLANV 236
Qy 291 VFFRCLLVQRCGGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALV 350
Db 237 VFFRCLLVQRCGGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALV 296
Qy 351 DIQLDHHERCDCICSSRRPR 370
Db 297 DIQLDHHERCDCICSSRRPR 316

RESULT 17

US-09-564-595D-57

; Sequence 57, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-57

Query Match 54.9%; Score 1095; DB 4; Length 303;
Best Local Similarity 67.4%; Pred. No. 1e-104;
Matches 213; Conservative 26; Mismatches 55; Indels 22; Gaps 5;
Qy 52 RDETIQVKGNGYVQSPRPNSYPNLLLTWRLHSOENTRIQLVFDNQFGLBEAENDICRY 111
Db 1 RDETIQVKGNGYVQSPRPNSYPNLLLTWRLHSOENTRIQLVFDNQFGLBEAENDICRY 60
Qy 112 DFVEVEDISETSTIIRGWCCHKEVPPRIKSRTNQIKITPKSDDYFVAKPGFKIYYSLE 171
Db 61 DFVEVEDISETSTIIRGWCCHKEVPPRIKSRTNQIKITPKSDDYFVAKPGFKIYYSLE 120
Qy 172 DFQPAASATNWSVTSSISGVSYNSPSVTDPTLIADALDKIAEFTVDDLKYFNPE 230
Db 121 DFQPAASV-----SPSVLPSPSALPLDLNNAITAFSTLEDLRYLEPE 164
Qy 231 SQWEDLENNYLDTPRYGRSY-HDKSK-VLDRLNDDAKRYSCCTPRNYSVNIREEKLA 288
Db 165 RWQLDLEDLRPTWQLLGKAFVGRKSRVVDLNLTEVRLYSCTPRNFSVIREELKRT 224
Qy 289 NVVFFRCLLVQRCGGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 348
Db 225 DTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP---KTGVRGLHKS 281
Qy 349 LVDIQLDHHERCDCIC 364
Db 282 LTDVALEHHEECDCVC 297

RESULT 18

US-09-564-595D-54
; Sequence 54, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04

```

; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; TYPE: PRT
; LENGTH: 302
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-5950-54

```

Query Match	53.28;	Score	1061.5;	DB	4;	Length	302;
Best Local Similarity	64.08;	Pred. No.	3e-101;				
Matches	206;	Conservative	36;	Mismatches	55;	Indels	25;
Gaps	6;						
QY	53	DETIQKNGYGVOSPREPNYSYPRNLLLTWRLHS-OENTRIQLVFDNOFGLEEANDICRY	111	:	:	:	:
Db	2	ERIIIVSTNGSIHSRPHPHYPRNTVLVWRLVAVEENWQLTFDERFGLEDDEDDICKY	61	:	:	:	:
QY	112	DFVEVEDISTTIIIRGRWGHKEVPPRIKSRNTQIKITPKSDDDYFVAKPGFKIYYSL-L	170	:	:	:	:
Db	62	DFVEVEEPSDGT--ILGRWCGSGTVPCQKIQKGNQIRIRFVSDSEYFFSEPGFCIHYNVM	119	:	:	:	:
QY	171	EDFQPAASATNWEVSTSSIGSVSYNSPSVTDPT-LIADALDKKIAEFDVTVEDLLKVFNP	229	:	:	:	:
Db	120	PQFTEAV-----SPSVLPFSALPLDLNNAITAFSTLEDLIRYLEP	160	:	:	:	:
QY	230	ESHQEDLENNYLDPTRYGRBSY-HDRKSKYDLDRLNDADAKRYSCTPPNYSVNITREELKLA	288	:	:	:	:
Db	161	ERWQLEDLYRPTWQLLKGAFVGRKSRVDRLNDADAKRYSCTPPNYSVNITREELKLA	220	:	:	:	:
QY	289	NVVFFPRCLLVQRCGNGCGGTNNWRSCTCNSGKTVKKYHEVLQFBPGCHKRGRAKTMA	348	:	:	:	:
Db	221	NVVFFPRCLLVQRCGNGCGGTNNWRSCTCNSGKTVKKYHEVLQFBPGCHKRGRAKTMA	280	:	:	:	:
QY	349	LVDIQLDHHERCDCICSSRRPPR	370	:	:	:	:
Db	281	LVDIQLDHHERCDCICSSRRPPR	302	:	:	:	:

```

RESULT 19
US-09-438-046-4
; Sequence 4, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTIN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D,
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 200
; TYPE: PR1
; ORGANISM: Homo sapiens

```

```

US-09-438-046-4

Query Match          49.2%; Score 982; DB 4; Length 200;
Best Local Similarity 96.8%; Pred. No. 2.7e-93;
Matches 181; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      184 ESVTSSISGVSNPSVTPDTLLIADALDKKIAEFDTVEDLLKYFNPESWOEDLENMYLDT 243
         |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      14 ESYTSSVSGYPNPSPTPTLLIADALDKKIAEFDTVEDLLKYFNPESWOEDLENMYLDT 73

QY      244 PRYGRGSYHDRKSVDLDRLNDDAKYSCTCPRYNSVNIREELKANVVFFPRCLLVORCG 303
         |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      74 PRYGRGSYHDRKSVDLDRLNDDAKYSCTCPRYNSVNIREELKANVVFFPRCLLVORCG 133

QY      304 GNGCGCTVMNRSTCNSGKTVKKYHYEVLPFGPHIKRRGRAKTMALVDIQLDHHIERCDCI 363
         |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      134 GNGCGCTVKLESCTCNSGKTVKKYHYEVLPFGPHIKRRGRAKTMALVDIQLDHHIERCDCI 193

QY      364 CSSRPPR 370
         |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      194 CSSRPPR 200

RESULT 20
US-09-457-066-43
; Sequence 43, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Fiddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-457-066-43

```

Query Match	37.7%;	Score	752;	DB	4;	Length	345;
Best Local Similarity	45.3%;	Pred. No.	4.1e-69;				
Matches	148;	Conservative	59;	Mismatches	92;	Indels	28;
Gaps	9;						
QY	42	ESNHLTDLYRRDDETIQVKGNGYVQSPFRFNPSYPRNLLLTWRLHS-CENTRIQLVFDNQFG	100				
Db	37	EQNGVQD-PRHREVVVISGNGSIHSKFPHTYPRNMVLVWRLVAVDENVRIQLTTFDRFG	95				
QY	101	LEEAEENDICRYDFVEVEDISETSTIIRGWCGHKEVPPRIKSTNQIKITFKSDDYFVAK	160				
Db	96	LEDPEDDICKYDFVEEVEEPSDGSVL--GRWCGSGTVPKQTSKGNHIRIRFVSDVEYFPE	153				
QY	161	PGFKIYYSILLEDPQAAASSETNWESVTSISGVSYNSPSVTDP-TLIADALDKKIAEFD	219				
Db	154	PGFCIHYSII---MPQVTTT-----SPSVLPSSSLDLJLNNAVTAFST	195				
QY	220	VEDLLKYFNPESQWEDLENNYLDTPYRGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNY	277				
Db	196	LEELIRYLEPDRQWDLDSLKYPTQWLLGKAFLYGGKSKVVNLLNLLKEEVKLYSCTPRNF	255				
QY	278	SVNIIREELKANVVFPRCLLTIVORCGNCCGCTVNNRSCCTNSGKTVKKYKHEVLQFPGH	337				
Db	256	SVSIIREELKRTDITFPGCLLVKRCGNCACCUHNCNECQVPRKTVKKYKHEVLQLRP--	313				
QY	338	IKRRGRAKTMALVDIQLDHHERCDCIC	364				

Db 314 -KTGVKGLHKS LTDV ALBHH EECDCVC 339

Search completed: November 10, 2005, 09:37:14
Job time : 46.9627 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:27:37 ; Search time 169.296 Seconds
(without alignments)
914.442 Million cell updates/sec

Title: US-10-606-055-2

Perfect score: 1994

Sequence: 1 MRLRLPVYLICANFCSCRD.....DIQLDHERCDCICSSRPPR 370

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications_AA.*

- 1: /cgn2_6/ptodata1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata1/pubpaa/US10F_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1994	100.0	370	9	US-09-823-033-5
2	1994	100.0	370	9	US-09-808-972-2
3	1994	100.0	370	9	US-09-915-582-56
4	1994	100.0	370	11	US-09-876-813-2
5	1994	100.0	370	11	US-09-833-245-1482
6	1994	100.0	370	13	US-10-086-623-8
7	1994	100.0	370	13	US-10-139-583-37
8	1994	100.0	370	13	US-10-039-847A-2
9	1994	100.0	370	14	US-10-260-539-8
10	1994	100.0	370	14	US-10-264-361-5
11	1994	100.0	370	14	US-10-258-557-2
					Sequence 5, Appli
					Sequence 2, Appli
					Sequence 56, Appl
					Sequence 2, Appli
					Sequence 1482, Ap
					Sequence 8, Appli
					Sequence 37, Appl
					Sequence 8, Appli
					Sequence 5, Appli
					Sequence 2, Appli

12	1994	100.0	370	14	US-10-226-559-2	Sequence 2, Appli
13	1994	100.0	370	14	US-10-274-638-2	Sequence 2, Appli
14	1994	100.0	370	14	US-10-011-364-4	Sequence 4, Appli
15	1994	100.0	370	14	US-10-277-802-56	Sequence 56, Appl
16	1994	100.0	370	15	US-10-246-091-8	Sequence 8, Appli
17	1994	100.0	370	15	US-10-365-095-2	Sequence 2, Appli
18	1994	100.0	370	15	US-10-321-962-4	Sequence 4, Appli
19	1994	100.0	370	15	US-10-606-055-2	Sequence 2, Appli
20	1994	100.0	370	15	US-10-664-432-5	Sequence 5, Appli
21	1994	100.0	370	16	US-10-284-2	Sequence 2, Appli
22	1994	100.0	370	16	US-10-664-432-5	Sequence 5, Appli
23	1994	100.0	370	16	US-10-877-623-2	Sequence 2, Appli
24	1994	100.0	370	16	US-10-772-927A-9	Sequence 9, Appli
25	1994	100.0	370	17	US-10-910-938-2	Sequence 2, Appli
26	1994	100.0	370	17	US-10-896-972-56	Sequence 56, Appl
27	1994	100.0	370	17	US-10-938-041-2	Sequence 2, Appli
28	1994	100.0	370	17	US-10-938-375-5	Sequence 5, Appli
29	1994	100.0	370	18	US-10-888-610-5	Sequence 5, Appli
30	1994	100.0	370	18	US-10-794-352-8	Sequence 8, Appli
31	1994	100.0	370	20	US-11-021-088-37	Sequence 37, Appl
32	1994	100.0	370	20	US-11-080-803-2	Sequence 2, Appli
33	1994	100.0	370	20	US-11-096-308-2	Sequence 2, Appli
34	1988	99.7	370	9	US-09-915-582-74	Sequence 74, Appl
35	1988	99.7	370	11	US-09-833-245-1481	Sequence 1481, Ap
36	1988	99.7	370	14	US-10-277-802-74	Sequence 74, Appl
37	1988	99.7	370	17	US-10-896-972-74	Sequence 74, Appl
38	1949	97.7	364	14	US-10-028-072-186	Sequence 186, App
39	1949	97.7	364	14	US-10-140-808-186	Sequence 186, App
40	1949	97.7	364	14	US-10-121-049-186	Sequence 186, App
41	1949	97.7	364	14	US-10-123-904-186	Sequence 186, App
42	1949	97.7	364	14	US-10-140-470-186	Sequence 186, App
43	1949	97.7	364	14	US-10-175-746-186	Sequence 186, App
44	1949	97.7	364	14	US-10-176-918-186	Sequence 186, App
45	1949	97.7	364	14	US-10-176-921-186	Sequence 186, App
46	1949	97.7	364	14	US-10-137-865-186	Sequence 186, App
47	1949	97.7	364	14	US-10-140-474-186	Sequence 186, App
48	1949	97.7	364	14	US-10-142-431-186	Sequence 186, App
49	1949	97.7	364	14	US-10-143-114-186	Sequence 186, App
50	1949	97.7	364	14	US-10-142-419-186	Sequence 186, App
51	1949	97.7	364	14	US-10-123-262-186	Sequence 186, App
52	1949	97.7	364	14	US-10-142-423-186	Sequence 186, App
53	1949	97.7	364	14	US-10-121-050-186	Sequence 186, App
54	1949	97.7	364	14	US-10-141-755-186	Sequence 186, App
55	1949	97.7	364	14	US-10-143-032-186	Sequence 186, App
56	1949	97.7	364	14	US-10-123-108-186	Sequence 186, App
57	1949	97.7	364	14	US-10-123-236-186	Sequence 186, App
58	1949	97.7	364	14	US-10-123-261-186	Sequence 186, App
59	1949	97.7	364	14	US-10-140-921-186	Sequence 186, App
60	1949	97.7	364	14	US-10-140-928-186	Sequence 186, App
61	1949	97.7	364	14	US-10-121-045-186	Sequence 186, App
62	1949	97.7	364	14	US-10-123-292-186	Sequence 186, App
63	1949	97.7	364	14	US-10-123-903-186	Sequence 186, App
64	1949	97.7	364	14	US-10-124-819-186	Sequence 186, App
65	1949	97.7	364	14	US-10-124-822-186	Sequence 186, App
66	1949	97.7	364	14	US-10-140-925-186	Sequence 186, App
67	1949	97.7	364	14	US-10-160-498-186	Sequence 186, App
68	1949	97.7	364	14	US-10-124-824-186	Sequence 186, App
69	1949	97.7	364	14	US-10-127-825A-186	Sequence 186, App
70	1949	97.7	364	14	US-10-127-829A-186	Sequence 186, App
71	1949	97.7	364	14	US-10-127-835A-186	Sequence 186, App
72	1949	97.7	364	14	US-10-127-839A-186	Sequence 186, App
73	1949	97.7	364	14	US-10-127-901A-186	Sequence 186, App
74	1949	97.7	364	14	US-10-128-693A-186	Sequence 186, App
75	1949	97.7	364	14	US-10-131-813A-186	Sequence 186, App
76	1949	97.7	364	14	US-10-131-818A-186	Sequence 186, App
77	1949	97.7	364	14	US-10-131-823A-186	Sequence 186, App
78	1949	97.7	364	14	US-10-131-824A-186	Sequence 186, App
79	1949	97.7	364	14	US-10-131-830A-186	Sequence 186, App
80	1949	97.7	364	14	US-10-131-837A-186	Sequence 186, App
81	1949	97.7	364	14	US-10-137-872A-186	Sequence 186, App
82	1949	97.7	364	14	US-10-147-500-186	Sequence 186, App
83	1949	97.7	364	14	US-10-147-502-186	Sequence 186, App
84	1949	97.7	364	14	US-10-147-515-186	Sequence 186, App

```
85 1949 97.7 364 14 US-10-147-517-186 Sequence 186, App
86 1949 97.7 364 14 US-10-147-526-186 Sequence 186, App
87 1949 97.7 364 14 US-10-147-527-186 Sequence 186, App
88 1949 97.7 364 14 US-10-121-041-186 Sequence 186, App
89 1949 97.7 364 14 US-10-121-043-186 Sequence 186, App
90 1949 97.7 364 14 US-10-121-047-186 Sequence 186, App
91 1949 97.7 364 14 US-10-123-215-186 Sequence 186, App
92 1949 97.7 364 14 US-10-123-902-186 Sequence 186, App
93 1949 97.7 364 14 US-10-123-908-186 Sequence 186, App
94 1949 97.7 364 14 US-10-123-909-186 Sequence 186, App
95 1949 97.7 364 14 US-10-123-910-186 Sequence 186, App
96 1949 97.7 364 14 US-10-124-813-186 Sequence 186, App
97 1949 97.7 364 14 US-10-124-817-186 Sequence 186, App
98 1949 97.7 364 14 US-10-125-922-186 Sequence 186, App
99 1949 97.7 364 14 US-10-125-924-186 Sequence 186, App
100 1949 97.7 364 14 US-10-140-860-186 Sequence 186, App
```

ALIGNMENTS

RESULT 1

```
US-09-823-033-5
; Sequence 5, Application US/09823033
; Patent No. US20020004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-5
```

```
Query Match 100.0%; Score 1994; DB 9; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRRDETIQVKG 60
DB 1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRRDETIQVKG 60

QY 61 NGYVQSPRFPNSYPRNLLLTWRLHSEQENTRIQLVFDNQFGLGEEAENDICRYDFVEVEDIS 120
DB 61 NGYVQSPRFPNSYPRNLLLTWRLHSEQENTRIQLVFDNQFGLGEEAENDICRYDFVEVEDIS 120

QY 121 ETSITIRGRWCCHKVEPPRIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLED FQPAASE 180
DB 121 ETSITIRGRWCCHKVEPPRIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLED FQPAASE 180

QY 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFPNPSWQEDLENNY 240
DB 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFPNPSWQEDLENNY 240

QY 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSC TPNYSVNIREELKLANVVFPPRCLLVQ 300
DB 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSC TPNYSVNIREELKLANVVFPPRCLLVQ 300

QY 301 RCGNCGCGTNNRSC TNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
DB 301 RCGNCGCGTNNRSC TNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370
```

RESULT 3

```
US-09-915-582-56
; Sequence 56, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
```

```
RESULT 2
US-09-808-972-2
; Sequence 2, Application US/09808972
; Patent No. US20020064832A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROBLASTIC
; FILE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-972-2
```

```
Query Match 100.0%; Score 1994; DB 9; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRRDETIQVKG 60
DB 1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRRDETIQVKG 60

QY 61 NGYVQSPRFPNSYPRNLLLTWRLHSEQENTRIQLVFDNQFGLGEEAENDICRYDFVEVEDIS 120
DB 61 NGYVQSPRFPNSYPRNLLLTWRLHSEQENTRIQLVFDNQFGLGEEAENDICRYDFVEVEDIS 120

QY 121 ETSITIRGRWCCHKVEPPRIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLED FQPAASE 180
DB 121 ETSITIRGRWCCHKVEPPRIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLED FQPAASE 180

QY 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFPNPSWQEDLENNY 240
DB 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFPNPSWQEDLENNY 240

QY 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSC TPNYSVNIREELKLANVVFPPRCLLVQ 300
DB 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSC TPNYSVNIREELKLANVVFPPRCLLVQ 300

QY 301 RCGNCGCGTNNRSC TNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
DB 301 RCGNCGCGTNNRSC TNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370
```

```
; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-582-56

Query Match      100.0%; Score 1994; DB 9; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLRYRDETIQVKG 60
DB      1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLRYRDETIQVKG 60

QY      61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
DB      61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120

QY      121 ETSIIIRGWCCHKEVPPRIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAAASE 180
DB      121 ETSIIIRGWCCHKEVPPRIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAAASE 180

QY      181 TWNESVTSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPSQOEDLENNY 240
DB      181 TWNESVTSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPSQOEDLENNY 240

QY      241 LDTPRYGRSYHDKRSKVDLRLNDDAKRYSCCTPRNYSVNIREEKLANVVFPPRCLLVQ 300
DB      241 LDTPRYGRSYHDKRSKVDLRLNDDAKRYSCCTPRNYSVNIREEKLANVVFPPRCLLVQ 300

QY      301 RCGNGCGGTVNRWCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
DB      301 RCGNGCGGTVNRWCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY      361 DCICSSRPPR 370
DB      361 DCICSSRPPR 370
```

RESULT 4

```
US-09-876-813-2
; Sequence 2, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG 2VEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-813-2

Query Match      100.0%; Score 1994; DB 11; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLRYRDETIQVKG 60
DB      1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLRYRDETIQVKG 60

QY      61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
DB      61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120

QY      121 ETSIIIRGWCCHKEVPPRIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAAASE 180
DB      121 ETSIIIRGWCCHKEVPPRIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAAASE 180

QY      181 TWNESVTSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPSQOEDLENNY 240
DB      181 TWNESVTSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPSQOEDLENNY 240

QY      241 LDTPRYGRSYHDKRSKVDLRLNDDAKRYSCCTPRNYSVNIREEKLANVVFPPRCLLVQ 300
DB      241 LDTPRYGRSYHDKRSKVDLRLNDDAKRYSCCTPRNYSVNIREEKLANVVFPPRCLLVQ 300

QY      301 RCGNGCGGTVNRWCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
DB      301 RCGNGCGGTVNRWCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY      361 DCICSSRPPR 370
DB      361 DCICSSRPPR 370
```

RESULT 5

```
US-09-833-245-1482
; Sequence 1482, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1482
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1482
```

```
Query Match      100.0%; Score 1994; DB 11; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLRYRDETIQVKG 60
DB      1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLRYRDETIQVKG 60

QY      61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
DB      61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
```

```
Db 61 NGYVQSPRPFPNSYPNNLLLTWRLHSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
QY 121 ETSTIIIRGWCHEVPPIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLEDFQPAASE 180
Db 121 ETSTIIIRGWCHEVPPIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLEDFQPAASE 180
QY 181 TNWESVTSISGSVNSPSTVDTPTLIADALDKKIAEFTVEDLLKYFNPESQEDLENNY 240
Db 181 TNWESVTSISGSVNSPSTVDTPTLIADALDKKIAEFTVEDLLKYFNPESQEDLENNY 240
QY 241 LDTPIRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Db 241 LDTPIRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREEKLANVVFPPRCLLVQ 300
QY 301 RCGNGCGGTVNNRSCCTNSGKTVKKYHEVLQFEPFGHIKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGNGCGGTVNNRSCCTNSGKTVKKYHEVLQFEPFGHIKRRGRKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 6
US-10-086-623-8
; Sequence 8, Application US/10086623
; Publication No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/086,623
; CURRENT FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-623-8

Query Match 100.0%; Score 1994; DB 13; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLI FVYTLICANFCSCRDTSATPQASIKALRNANLRDES NHLTDL YRRDET I QVKG 60
Db 1 MHRLI FVYTLICANFCSCRDTSATPQASIKALRNANLRDES NHLTDL YRRDET I QVKG 60

QY 61 NGYVQSPRPFPNSYPNNLLLTWRLHSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPFPNSYPNNLLLTWRLHSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120

QY 121 ETSTIIIRGWCHEVPPIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLEDFQPAASE 180
Db 121 ETSTIIIRGWCHEVPPIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLEDFQPAASE 180
QY 181 TNWESVTSISGSVNSPSTVDTPTLIADALDKKIAEFTVEDLLKYFNPESQEDLENNY 240
Db 181 TNWESVTSISGSVNSPSTVDTPTLIADALDKKIAEFTVEDLLKYFNPESQEDLENNY 240
QY 241 LDTPIRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Db 241 LDTPIRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREEKLANVVFPPRCLLVQ 300
QY 301 RCGNGCGGTVNNRSCCTNSGKTVKKYHEVLQFEPFGHIKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGNGCGGTVNNRSCCTNSGKTVKKYHEVLQFEPFGHIKRRGRKTMALVDIQLDHHERC 360
```

```
QY 121 ETSTIIIRGWCHEVPPIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLEDFQPAASE 180
Db 121 ETSTIIIRGWCHEVPPIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLEDFQPAASE 180
QY 181 TNWESVTSISGSVNSPSTVDTPTLIADALDKKIAEFTVEDLLKYFNPESQEDLENNY 240
Db 181 TNWESVTSISGSVNSPSTVDTPTLIADALDKKIAEFTVEDLLKYFNPESQEDLENNY 240
QY 241 LDTPIRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Db 241 LDTPIRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREEKLANVVFPPRCLLVQ 300
QY 301 RCGNGCGGTVNNRSCCTNSGKTVKKYHEVLQFEPFGHIKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGNGCGGTVNNRSCCTNSGKTVKKYHEVLQFEPFGHIKRRGRKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 7
US-10-139-583-37
; Sequence 37, Application US/10139583
; Publication No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-583-37

Query Match 100.0%; Score 1994; DB 13; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLI FVYTLICANFCSCRDTSATPQASIKALRNANLRDES NHLTDL YRRDET I QVKG 60
Db 1 MHRLI FVYTLICANFCSCRDTSATPQASIKALRNANLRDES NHLTDL YRRDET I QVKG 60

QY 61 NGYVQSPRPFPNSYPNNLLLTWRLHSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPFPNSYPNNLLLTWRLHSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120

QY 121 ETSTIIIRGWCHEVPPIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLEDFQPAASE 180
Db 121 ETSTIIIRGWCHEVPPIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLEDFQPAASE 180
QY 181 TNWESVTSISGSVNSPSTVDTPTLIADALDKKIAEFTVEDLLKYFNPESQEDLENNY 240
Db 181 TNWESVTSISGSVNSPSTVDTPTLIADALDKKIAEFTVEDLLKYFNPESQEDLENNY 240
QY 241 LDTPIRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Db 241 LDTPIRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREEKLANVVFPPRCLLVQ 300
QY 301 RCGNGCGGTVNNRSCCTNSGKTVKKYHEVLQFEPFGHIKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGNGCGGTVNNRSCCTNSGKTVKKYHEVLQFEPFGHIKRRGRKTMALVDIQLDHHERC 360
```


Db 301 RCGNCGGTGTVNRSTCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHRC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 8

US-10-039-847A-2
; Sequence 2, Application US/10039847A
; Publication No. US20020183273A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; TITLE OF INVENTION: KIDNEY FUNCTION
; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039,847A
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-847A-2

Query Match 100.0%; Score 1994; DB 13; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRSNHLTDLRRDETTQVKG 60
Db 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRSNHLTDLRRDETTQVKG 60
Qy 61 NGVQSPFPNSYPNLLTWRHLSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGVQSPFPNSYPNLLTWRHLSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Qy 121 ETSIIIRGWCHEKVPPIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSIIIRGWCHEKVPPIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Qy 181 TWESVTSSISGVSNPSVTDPTLIADALDKKIAEFTDVEDLLKYFNPSQEDLENNY 240
Db 181 TWESVTSSISGVSNPSVTDPTLIADALDKKIAEFTDVEDLLKYFNPSQEDLENNY 240
Qy 241 LDPYRGRSYHDKRSKVDLRLNDDAKRYSCPTPNYSVNIREEKLANVFPFRCCLLVQ 300
Db 241 LDPYRGRSYHDKRSKVDLRLNDDAKRYSCPTPNYSVNIREEKLANVFPFRCCLLVQ 300
Qy 301 RCGNCGGTGTVNRSTCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHRC 360
Db 301 RCGNCGGTGTVNRSTCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHRC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 9

US-10-260-539-8
; Sequence 8, Application US/10260539
; Publication No. US20030073637A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: Li, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko

; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES T
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/260,539
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-260-539-8

Query Match 100.0%; Score 1994; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRSNHLTDLRRDETTQVKG 60
Db 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRSNHLTDLRRDETTQVKG 60
Qy 61 NGVQSPFPNSYPNLLTWRHLSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGVQSPFPNSYPNLLTWRHLSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Qy 121 ETSIIIRGWCHEKVPPIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSIIIRGWCHEKVPPIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Qy 181 TWESVTSSISGVSNPSVTDPTLIADALDKKIAEFTDVEDLLKYFNPSQEDLENNY 240
Db 181 TWESVTSSISGVSNPSVTDPTLIADALDKKIAEFTDVEDLLKYFNPSQEDLENNY 240
Qy 241 LDPYRGRSYHDKRSKVDLRLNDDAKRYSCPTPNYSVNIREEKLANVFPFRCCLLVQ 300
Db 241 LDPYRGRSYHDKRSKVDLRLNDDAKRYSCPTPNYSVNIREEKLANVFPFRCCLLVQ 300
Qy 301 RCGNCGGTGTVNRSTCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHRC 360
Db 301 RCGNCGGTGTVNRSTCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHRC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 10

US-10-264-361-5
; Sequence 5, Application US/10264361
; Publication No. US20030087870A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/264,361

```
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/695,121
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-361-5

Query Match      100.0%; Score 1994; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFYVTLICANFCSCRDTSATPQSASIKALRNANLRRDESNNHLTDLYRRDETIQVG 60
Db 1 MHRLLFYVTLICANFCSCRDTSATPQSASIKALRNANLRRDESNNHLTDLYRRDETIQVG 60
Qy 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAEENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAEENDICRYDFVEVEDIS 120
Qy 121 ETSTIIIRGWCHEVPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLLEDFOPAAASE 180
Db 121 ETSTIIIRGWCHEVPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLLEDFOPAAASE 180
Qy 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSWQEDLENNY 240
Db 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSWQEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREELKLANVVFPRCLLVQ 300
Db 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREELKLANVVFPRCLLVQ 300
Qy 301 RCGNCGCGTVNWSCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMAVDIQLDHHERC 360
Db 301 RCGNCGCGTVNWSCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMAVDIQLDHHERC 360
Qy 361 DCICSSRP 370
Db 361 DCICSSRP 370

RESULT 12
US-10-226-559-2
; Sequence 2, Application US/10226559
; Publication No. US20030105015A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/10/226,559
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US/09/540,224
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-226-559-2

Query Match      100.0%; Score 1994; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFYVTLICANFCSCRDTSATPQSASIKALRNANLRRDESNNHLTDLYRRDETIQVG 60
Db 1 MHRLLFYVTLICANFCSCRDTSATPQSASIKALRNANLRRDESNNHLTDLYRRDETIQVG 60
Qy 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAEENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAEENDICRYDFVEVEDIS 120
Qy 121 ETSTIIIRGWCHEVPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLLEDFOPAAASE 180
Db 121 ETSTIIIRGWCHEVPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLLEDFOPAAASE 180
Qy 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSWQEDLENNY 240
Db 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSWQEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREELKLANVVFPRCLLVQ 300
```

Db 241 LPTPRGRSYHDKSKVDLRDLNDADAKRYCTPRNYSVNIIEELKLANVFFPRCLLVQ 300
QY 301 RCGGCGCGTVNWRSTCNSTGKTVKKYHEVLOFEPGHKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGGCGCGTVNWRSTCNSTGKTVKKYHEVLOFEPGHKRRGRKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 13

US-10-274-638-2
; Sequence 2, Application US/10274638
; Publication No. US20030109000A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIZED GROWTH FACTOR AND MATERIALS
; FILE REFERENCE: 01-30
; CURRENT APPLICATION NUMBER: US/10/274,638
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 60/346,117
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-274-638-2

Query Match 100.0%; Score 1994; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167; Mismatches 0; Indels 0; Gaps 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLYRDETIQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLYRDETIQVKG 60
QY 61 NGVQSPRPNSYPNLLLTWRLHSEENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGVQSPRPNSYPNLLLTWRLHSEENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
QY 121 ETSTIIRGWCCHKEVPPRIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSTIIRGWCCHKEVPPRIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
QY 181 TWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPEMQEDLENNY 240
Db 181 TWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPEMQEDLENNY 240
QY 241 LPTPRGRSYHDKSKVDLRDLNDADAKRYCTPRNYSVNIIEELKLANVFFPRCLLVQ 300
Db 241 LPTPRGRSYHDKSKVDLRDLNDADAKRYCTPRNYSVNIIEELKLANVFFPRCLLVQ 300
QY 301 RCGGCGCGTVNWRSTCNSTGKTVKKYHEVLOFEPGHKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGGCGCGTVNWRSTCNSTGKTVKKYHEVLOFEPGHKRRGRKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 14

US-10-011-364-4
; Sequence 4, Application US/10011364
; Publication No. US20030153495A1
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henry

; APPLICANT: Jeffers, Michael
; APPLICANT: Shimkets, Richard
; APPLICANT: Pravaga, Sudhirdas
; APPLICANT: Boldog, Ferenc
; APPLICANT: Yang, Meijia
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Rittman, B.
; APPLICANT: Shimkets, Juliette
; APPLICANT: LaRoche, William
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease Using Growth
; FILE REFERENCE: 15966-557A IBD CIP
; CURRENT APPLICATION NUMBER: US/10/011,364
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/246,206
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 09/992,840
; PRIOR FILING DATE: 2001-11-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-364-4

Query Match 100.0%; Score 1994; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167; Mismatches 0; Indels 0; Gaps 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLYRDETIQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLYRDETIQVKG 60
QY 61 NGVQSPRPNSYPNLLLTWRLHSEENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGVQSPRPNSYPNLLLTWRLHSEENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
QY 121 ETSTIIRGWCCHKEVPPRIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSTIIRGWCCHKEVPPRIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
QY 181 TWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPEMQEDLENNY 240
Db 181 TWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPEMQEDLENNY 240
QY 241 LPTPRGRSYHDKSKVDLRDLNDADAKRYCTPRNYSVNIIEELKLANVFFPRCLLVQ 300
Db 241 LPTPRGRSYHDKSKVDLRDLNDADAKRYCTPRNYSVNIIEELKLANVFFPRCLLVQ 300
QY 301 RCGGCGCGTVNWRSTCNSTGKTVKKYHEVLOFEPGHKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGGCGCGTVNWRSTCNSTGKTVKKYHEVLOFEPGHKRRGRKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 15

US-10-277-802-56
; Sequence 56, Application US/10277802
; Publication No. US20030190707A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/10/277,802
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 09/915,582
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431

```
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 56
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-277-802-56

Query Match      100.0%; Score 1994; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDESNNHLLTDLRRDETIOVKG 60
Db  1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDESNNHLLTDLRRDETIOVKG 60

Qy  61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS 120
Db  61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS 120

Qy  121 ETSTIIIRGWCHEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
Db  121 ETSTIIIRGWCHEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180

Qy  181 TNWESVTSISGVSYNPSVTDPTLIADALDKKTAEDFTVEDLLKYFNPSQWQEDLENNY 240
Db  181 TNWESVTSISGVSYNPSVTDPTLIADALDKKTAEDFTVEDLLKYFNPSQWQEDLENNY 240

Qy  241 LDTPRYGRSYHDKRSKVDLDRNDADAKRYSCCTPRNYSVNIREEELKLANVVFVFFPRCLLVQ 300
Db  241 LDTPRYGRSYHDKRSKVDLDRNDADAKRYSCCTPRNYSVNIREEELKLANVVFVFFPRCLLVQ 300

Qy  301 RCGNCGCGTVNWRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERC 360
Db  301 RCGNCGCGTVNWRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERC 360

Qy  361 DCICSSRRP 370
Db  361 DCICSSRRP 370

RESULT 16
US-10-246-091-8
; Sequence 8, Application US/10246091
; Publication No. US20030203844A1
; GENERAL INFORMATION:
; APPLICANT: Delfani, Khoumars
; APPLICANT: Janson, Ann Marie
; APPLICANT: Kuhn, Georg
; APPLICANT: Plate, Karlheinz
; APPLICANT: Schnazer, Anne
; APPLICANT: Wachs, Frank-Peter
; APPLICANT: Zhao, Ming
; TITLE OF INVENTION: Treatment of Central Nervous System Disorders
; FILE REFERENCE: 21882-504 (PGF/VEGF)
; CURRENT APPLICATION NUMBER: US/10/246,091
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,381
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/326,044
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-246-091-8

Query Match      100.0%; Score 1994; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDESNNHLLTDLRRDETIOVKG 60
Db  1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDESNNHLLTDLRRDETIOVKG 60

Qy  61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS 120
Db  61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS 120

Qy  121 ETSTIIIRGWCHEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
Db  121 ETSTIIIRGWCHEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180

Qy  181 TNWESVTSISGVSYNPSVTDPTLIADALDKKTAEDFTVEDLLKYFNPSQWQEDLENNY 240
Db  181 TNWESVTSISGVSYNPSVTDPTLIADALDKKTAEDFTVEDLLKYFNPSQWQEDLENNY 240

Qy  241 LDTPRYGRSYHDKRSKVDLDRNDADAKRYSCCTPRNYSVNIREEELKLANVVFVFFPRCLLVQ 300
Db  241 LDTPRYGRSYHDKRSKVDLDRNDADAKRYSCCTPRNYSVNIREEELKLANVVFVFFPRCLLVQ 300

Qy  301 RCGNCGCGTVNWRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERC 360
Db  301 RCGNCGCGTVNWRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERC 360

Qy  361 DCICSSRRP 370
Db  361 DCICSSRRP 370

RESULT 17
US-10-365-095-2
; Sequence 2, Application US/10365095
; Publication No. US20030224488A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Moore, Margaret D.
; APPLICANT: Swiderek, Kristine M.
; APPLICANT: Birks, Carl W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR PREPARING DIMERIC GROWTH FACTORS
; FILE REFERENCE: 01-33
; CURRENT APPLICATION NUMBER: US/10/365,095
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 60/355,882
; PRIOR FILING DATE: 2002-02-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-365-095-2

Query Match      100.0%; Score 1994; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDESNNHLLTDLRRDETIOVKG 60
Db  1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDESNNHLLTDLRRDETIOVKG 60

Qy  61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS 120
Db  61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS 120

Qy  121 ETSTIIIRGWCHEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
Db  121 ETSTIIIRGWCHEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
```

```
Db 121 ETSTIIRGWCHEKVPVPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLEDQPPAAASE 180
Qy 181 TWNESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDVTDVLLKYFNPESWQEDLENNY 240
Db 181 TWNESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDVTDVLLKYFNPESWQEDLENNY 240
Qy 241 LOTPRYGRGSYHDRKSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Db 241 LOTPRYGRGSYHDRKSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Qy 301 RCGNGCGCTVNWRSCTCNSGKTVKKYHEVLOFEPGHIKRRGRKTMALVDIOLDHHERC 360
Db 301 RCGNGCGCTVNWRSCTCNSGKTVKKYHEVLOFEPGHIKRRGRKTMALVDIOLDHHERC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 18
US-10-321-962-4
; Sequence 4, Application US/10321962
; Publication No. US20040006015A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Fernandes, Elma
; APPLICANT: Jeffers, Michael E.
; APPLICANT: LaRochele, William J.
; APPLICANT: Lichenstein, Henry S.
; APPLICANT: Peterson, Jeffrey
; APPLICANT: Prayaga, Suchirdas
; APPLICANT: Rittman, Beth
; APPLICANT: Shimkets, Juliette
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Yang, Meijia
; APPLICANT: Curagen Corporation
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease
; FILE REFERENCE: Using Growth Factors
; CURRENT APPLICATION NUMBER: US/10/321,962
; CURRENT FILING DATE: 2002-12-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-962-4

Query Match 100.0%; Score 1994; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLYRRDETIQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLYRRDETIQVKG 60
Qy 61 NGYVQSPFPNSYPNLLLTWRLHSEOENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPFPNSYPNLLLTWRLHSEOENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Qy 121 ETSTIIRGWCHEKVPVPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLEDQPPAAASE 180
Db 121 ETSTIIRGWCHEKVPVPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLEDQPPAAASE 180
Qy 181 TWNESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDVTDVLLKYFNPESWQEDLENNY 240
Db 181 TWNESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDVTDVLLKYFNPESWQEDLENNY 240
Qy 241 LOTPRYGRGSYHDRKSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Db 241 LOTPRYGRGSYHDRKSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Qy 301 RCGNGCGCTVNWRSCTCNSGKTVKKYHEVLOFEPGHIKRRGRKTMALVDIOLDHHERC 360
Db 301 RCGNGCGCTVNWRSCTCNSGKTVKKYHEVLOFEPGHIKRRGRKTMALVDIOLDHHERC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370
```

```
Qy 301 RCGNGCGCTVNWRSCTCNSGKTVKKYHEVLOFEPGHIKRRGRKTMALVDIOLDHHERC 360
Db 301 RCGNGCGCTVNWRSCTCNSGKTVKKYHEVLOFEPGHIKRRGRKTMALVDIOLDHHERC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 19
US-10-606-055-2
; Sequence 2, Application US/10606055
; Publication No. US20040043027A1
; GENERAL INFORMATION:
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/10/606,055
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US/09/808,972
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-606-055-2

Query Match 100.0%; Score 1994; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLYRRDETIQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLYRRDETIQVKG 60
Qy 61 NGYVQSPFPNSYPNLLLTWRLHSEOENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPFPNSYPNLLLTWRLHSEOENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Qy 121 ETSTIIRGWCHEKVPVPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLEDQPPAAASE 180
Db 121 ETSTIIRGWCHEKVPVPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLEDQPPAAASE 180
Qy 181 TWNESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDVTDVLLKYFNPESWQEDLENNY 240
Db 181 TWNESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDVTDVLLKYFNPESWQEDLENNY 240
Qy 241 LOTPRYGRGSYHDRKSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Db 241 LOTPRYGRGSYHDRKSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Qy 301 RCGNGCGCTVNWRSCTCNSGKTVKKYHEVLOFEPGHIKRRGRKTMALVDIOLDHHERC 360
Db 301 RCGNGCGCTVNWRSCTCNSGKTVKKYHEVLOFEPGHIKRRGRKTMALVDIOLDHHERC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370
```

Db 361 DCICSSRRPR 370

RESULT 20

US-10-664-432-5
; Sequence 5, Application US/10664432
; Publication No. US20040043031A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/10/664,432
; CURRENT FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-432-5

Query Match 100.0%; Score 1994; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFVYTLICANFCSCRDTSATQASIKALRNANLRRDESNHLTDLYRRDETIQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATQASIKALRNANLRRDESNHLTDLYRRDETIQVKG 60
QY 61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLSEAEENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLSEAEENDICRYDFVEVEDIS 120
QY 121 ETSTIIRGRWCCHKVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLLEDFQAAAASE 180
Db 121 ETSTIIRGRWCCHKVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLLEDFQAAAASE 180
QY 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSQWEDLENNY 240
Db 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSQWEDLENNY 240
QY 241 LDTPRYGRSYHDRKSKVDLRLNDADAKRYSCTPRNSYNIREELKLANVVFPPRCLLVQ 300
Db 241 LDTPRYGRSYHDRKSKVDLRLNDADAKRYSCTPRNSYNIREELKLANVVFPPRCLLVQ 300
QY 301 RCGGNCGCCTVNRSCCTNSGKTVKKYHEVLQFEPFGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGGNCGCCTVNRSCCTNSGKTVKKYHEVLQFEPFGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

Search completed: November 10, 2005, 09:41:02
Job time : 172.296 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:24:01 ; Search time 39.0683 Seconds
(without alignments)
911.229 Million cell updates/sec

Title: US-10-606-055-2

Perfect score: 1994

Sequence: 1 MHRLIFVYTLICANFCSCRD.....DIQLDHERCDCICSSRPPR 370

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first-100 summaries

Database :

PIR 79:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1988	99.7	370	2	spinal cord-derive
2	1775	89.0	370	2	spinal cord-derive
3	1737	87.1	370	2	platelet-derived g
4	1933	9.7	823	1	procollagen C-endo
5	189.5	9.5	707	2	procollagen C-endo
6	187.5	9.4	730	1	procollagen C-endo
7	187.5	9.4	986	1	procollagen C-endo
8	187.5	9.4	991	2	procollagen C-endo
9	184.5	9.3	3623	2	intrinsic factor-B
10	176	8.8	927	1	A5 antigen precurs
11	174.5	8.8	1057	1	dorsal-ventral pat
12	173	8.7	3623	2	intrinsic factor-B
13	161	8.1	579	2	membrane-type friz
14	156.5	7.8	1524	2	polyporetein - Afri
15	153	7.7	1464	2	development protei
16	149	7.5	1070	2	colloid-BMP-1 like
17	148	7.4	686	1	Ra-reactive factor
18	144	7.2	2403	2	sanko - human
19	143	7.2	699	1	Ra-reactive factor
20	141.5	7.1	767	2	hypothetical prote
21	138.5	6.9	1004	2	oviductin [EC 3.4.
22	137.5	6.9	3871	2	hypothetical prote
23	137	6.9	276	2	TSG-6 homolog PS4
24	136.5	6.8	449	2	procollagen I C-pr
25	136.5	6.8	597	2	metalloproteinase
26	134	6.7	705	1	complement subcomp
27	130.5	6.5	402	2	procollagen I C-pr
28	129	6.5	277	2	hyaluronate-bindin
29	125.5	6.3	533	2	brain-specific CUB

tumor necrosis fac
ebnerin precursor
hypothetical prote
vascular endotheli
hypothetical prote
complement subcomp
enteropeptidase (E
complement subcomp
hennin - rabbit
enteropeptidase (E
mucin (clone pCM31
complement subcomp
hypothetical prote
CRP-ductin-alpha p
variant-specific s
membrane-bound arg
UVS.2 protein - Af
hypothetical prote
conserved hypotet
hypothetical prote
probable pili asem
hypothetical prote
alkaline phosphata
hypothetical prote
16K vascular endot
hypothetical prote
hypothetical prote
surface-located me
hypothetical prote
hypothetical prote
hypothetical prote
hemoglobin recepto
hypothetical prote
variant-specific s
platelet-derived g
platelet-derived g
probable type-I se
HLVD secretion pro
hypothetical prote
platelet-derived g
hypothetical prote
hypothetical prote
lipoprotein (impor
protein maturation
hypothetical prote
variant-specific s
probable membrane
vascular endotheli
hypothetical prote
hypothetical prote
outer capsid prote
hypothetical prote
calreticulin precu
DNA-directed DNA p
DNA polymerase orf
hypothetical prote
platelet-derived g
hypothetical prote
Fe-S oxidoreductas
LIM domain protein
hypothetical prote
hercz protein - mo
protein B0454.7 [i
related to tol pro
hypothetical prote
hypothetical prote

Db 121 ESSTVVRGRWCGHKEIPRITSRNQKITFKSDYFAKPGFKITYSFEVDEQPEASE 180
QY 181 TNNESVTSISGVSYSNPSVTDPTLLADALDKIAEDTVEDLLKFNPSNEDLENNY 240
Db 181 TNNESVTSISGVSYSNPSVTDPTLLADALDKIAEDTVEDLLKFNPSNEDLENNY 240
QY 241 LDPFRGRGRSYHNRKSKVDLDRNLNDADAKRSCPTPRNSVNIREEKLAVNFFPRCLVQ 300
Db 241 LDPFRGRGRSYHNRKSKVDLDRNLNDADAKRSCPTPRNSVNIREEKLAVNFFPRCLVQ 300
QY 301 RCGNGCGCTVMNRSGCTCNVKKYHEVLQEPGHIKRRGRAKTALVDIQLDHHERC 360
Db 301 RCGNGCGCTVMNRSGCTCNVKKYHEVLQEPGHIKRRGRAKTALVDIQLDHHERC 360
QY 361 DCTCSSRPPR 370
Db 361 DCTCSSRPPR 370

RESULT 4

A:Accession: A58788
A:Residues: 1-702, EKRPALQPPRRGHQKFRVQKRNTPQ' <MOZ>
A:Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
R:Takehara, K.; Lyons, G.E.; Greenspan, D.S.
J:BioL. Chem. 269, 32572-32578, 1994.
A:Title: Bone morphogenetic protein-1 and a mammalian tollold homologue (lmlid) are encoded
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: A37278
A:Residues: 1-707 <MAE>
A:Cross-references: UNIPROT:P98070; GB:112249; NID:G406540; PIDN:AAA16313.1; PID:G40654
C:Comment: This protein induces ectopic cartilage formation in vivo.
C:Superfamily: procollagen C-endopeptidase; ascatin homology; Ctr/Cls repeat homology;
C:Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
F:93-284/Domain: ascatin homology <AST>
F:285-397/Region: complement lr/ls-like repeat
F:285-394/Domain: Ctr/Cls repeat homology <CLR1>
F:388-510/Region: complement lr/ls-like repeat
F:398-507/Domain: Ctr/Cls repeat homology <CLR2>
F:514-550/Domain: EGF homology <EGF>
F:554-666/Region: complement lr/ls-like repeat
F:62-105,295,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:176,180,186,235/Binding site: zinc (His, His, Tyr) #status predicted
F:177/Active site: Glu #status predicted
F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

A:Molecule type: mRNA
A:Residues: 1-702, EKRPALQPPRRGHQKFRVQKRNTPQ' <MOZ>
A:Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
R:Takehara, K.; Lyons, G.E.; Greenspan, D.S.
J:BioL. Chem. 269, 32572-32578, 1994.
A:Title: Bone morphogenetic protein-1 and a mammalian tollold homologue (lmlid) are encoded
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: A58788
A:Molecule type: mRNA
A:Residues: 703-823 <TAK>
A:Cross-references: GB:L35278; NID:G619423; PIDN:AA41703.1; PID:G619424
C:Genetics:
A:Gene: GDB:BMPI, BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; ascatin homology; Ctr/Cls repeat homology;
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g1
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-823/Product: procollagen C-endopeptidase splice form His #status predicted <MAT>
F:322-431/Domain: ascatin homology <AST>
F:432-544/Domain: Ctr/Cls repeat homology <CLR1>
F:551-587/Domain: EGF homology <EGF>
F:591-700/Domain: Ctr/Cls repeat homology <CLR2>
F:738-752/Region: histidine-rich
F:91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,272/Binding site: zinc (His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.7%; Score 193; DB 1; Length 823;
Best Local Similarity 28.7%; Pred. No. 1.5e-06;
Matches 71; Conservative 33; Mismatches 89; Indels 54; Gaps 11;
QY 59 KNGVYQSPFPNSYPNNLLTWRLHSOENTRIQLVFNDFGLBEANDICRDPVEVED 118
Db 597 KNGVYQSPFPNSYPNNLLTWRLHSOENTRIQLVFNDFGLBEANDICRDPVEVED 118

QY 119 ISETSTIRGRWCGHKEVPRIRKSRNQKITFKSDYFAKPGFKIYSSYLE----- 171
Db 654 GLTADSKLHGKFCG-SEKEPVITSQYNNMKRVEKSDN-TYSSKGFQAHFVSVEGAGDRH 711
QY 172 -----DFOPAASETNWESVTSISGVSYSNPSVTD---PTLLADALD 211
Db 712 SHLSGELLLCPHALVDTPAPSPALSHGDPHATHTHVHCHPCIAOTCRGPELGASRLS 771
QY 212 KRIAEFDYEDLLKFNPSNEDLENNYTD-TPRRGRGRSYHNRKSKVDLDRNLNDADAKRY 270
Db 772 PQPGHLLTIA-----PQ-----EGSYLDFWDTIRG-----DPKPR---RRRKSUKTF 810
QY 271 SCTPRNY 277
Db 811 SLTPATF 817

RESULT 5

A:Accession: JC2218
A:Residues: 1-707 <MAE>
A:Cross-references: UNIPROT:P98070; GB:112249; NID:G406540; PIDN:AAA16313.1; PID:G40654
C:Comment: This protein induces ectopic cartilage formation in vivo.
C:Superfamily: procollagen C-endopeptidase; ascatin homology; Ctr/Cls repeat homology;
C:Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
F:93-284/Domain: ascatin homology <AST>
F:285-397/Region: complement lr/ls-like repeat
F:285-394/Domain: Ctr/Cls repeat homology <CLR1>
F:388-510/Region: complement lr/ls-like repeat
F:398-507/Domain: Ctr/Cls repeat homology <CLR2>
F:514-550/Domain: EGF homology <EGF>
F:554-666/Region: complement lr/ls-like repeat
F:62-105,295,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:176,180,186,235/Binding site: zinc (His, His, Tyr) #status predicted
F:177/Active site: Glu #status predicted
F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

A:Molecule type: mRNA
A:Residues: 1-707 <MAE>
A:Cross-references: UNIPROT:P98070; GB:112249; NID:G406540; PIDN:AAA16313.1; PID:G40654
C:Comment: This protein induces ectopic cartilage formation in vivo.
C:Superfamily: procollagen C-endopeptidase; ascatin homology; Ctr/Cls repeat homology;
C:Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
F:93-284/Domain: ascatin homology <AST>
F:285-397/Region: complement lr/ls-like repeat
F:285-394/Domain: Ctr/Cls repeat homology <CLR1>
F:388-510/Region: complement lr/ls-like repeat
F:398-507/Domain: Ctr/Cls repeat homology <CLR2>
F:514-550/Domain: EGF homology <EGF>
F:554-666/Region: complement lr/ls-like repeat
F:62-105,295,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:176,180,186,235/Binding site: zinc (His, His, Tyr) #status predicted
F:177/Active site: Glu #status predicted
F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.5%; Score 189.5; DB 2; Length 707;
Best Local Similarity 42.5%; Pred. No. 2.2e-06;
Matches 45; Conservative 18; Mismatches 38; Indels 5; Gaps 4;
QY 59 KNGVYQSPFPNSYPNNLLTWRLHSOENTRIQLVFNDFGLBEANDICRDPVEVED 118
Db 560 KNGVYQSPFPNSYPNNLLTWRLHSOENTRIQLVFNDFGLBEANDICRDPVEVED 118
QY 119 ISETSTIRGRWCGHKEVPRIRKSRNQKITFKSDYFAKPGFK 164
Db 617 GLTADSKLHGKFCG-SEPAVITISQYNNMKRVEKSDN-TYSSKGFQ 660

RESULT 6

A:Accession: A37278
A:Residues: 1-702, EKRPALQPPRRGHQKFRVQKRNTPQ' <MOZ>
A:Cross-references: UNIPROT:P98070; GB:112249; NID:G406540; PIDN:AAA16313.1; PID:G40654
C:Comment: This protein induces ectopic cartilage formation in vivo.
C:Superfamily: procollagen C-endopeptidase; ascatin homology; Ctr/Cls repeat homology;
C:Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
F:93-284/Domain: ascatin homology <AST>
F:285-397/Region: complement lr/ls-like repeat
F:285-394/Domain: Ctr/Cls repeat homology <CLR1>
F:388-510/Region: complement lr/ls-like repeat
F:398-507/Domain: Ctr/Cls repeat homology <CLR2>
F:514-550/Domain: EGF homology <EGF>
F:554-666/Region: complement lr/ls-like repeat
F:62-105,295,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:176,180,186,235/Binding site: zinc (His, His, Tyr) #status predicted
F:177/Active site: Glu #status predicted
F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

A: Molecule type: mRNA
A: Residues: 1-730 <MOZ>
A: Cross-references: GB:M22486; NID:gi79499; PIDD:AAA5193.1; PID:gi79500
C: Geneticks:
A: Gene: GDB: BMP1
A: Cross-references: GDB:125203; OMIM:112264
A: Map position: 8p21-8p21
C: Function:
A: Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type I
C: Superfamily: procollagen C-endopeptidase; asctatin homology: C1r/C1s repeat homology; E
C: Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:1-22/Domain: signal sequence #status predicted <SIG>
F:123-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>
F:130-321/Domain: astactin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EGF>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:91-142,332,363,599/Binding site: carboxylate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-387,435-461,488-510,551-563,559-572,574-587,591-617,644-666
F:211,217,223,572/Binding site: zinc (His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.4%; Score 187.5; DB 1; Length 730;
Best Local Similarity 39.4%; Pred. No. 3.3e-06;
Matches 43; Conservative 18; Mismatches 43; Indels 5; Gaps 3;

	QY	DG	DB	QY	DG	DB
59	KANGVQSPRPENPSPPRNLTLTWRLHSEENTRIQLVPDNGFGLAEANDICRPDYVED	118	597	KLNGSITSPGPKEPPEPNKNCIWLVAFTQYRISLPQD---FFETGBGDVCKDPFVEVR	653	
119	ISETSTIRGRWGCHKEVPRPKASTNIOIKTEKSDDVFAKKPPKIYY	167	654	GLTADSKLHGFCG-SSEKPEVITSSQNNMRPFESDN-TVSKECFKFAP	700	

RESULT 7
B58788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - human
N/Alternate names: bone morphogenic protein 1, tolloid-like splice form
C/Species: Homo sapiens (man)
C/Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004
C/Accession: AJ37278; B58788
R/Mozney, J.M.; Rosen, V.; Celeste, A.J.; Micsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A/Title: Novel regulators of bone formation: molecular clones and activities.
A/Reference number: AJ37278; MUID:89072730; PMID:3201241
A/Accession: AJ37278
A/Molecule type: mRNA
A/Residues: 1-702, 'EKRPALQPRGRGHQLEKRYQKRRTPQ' <NOZ>
A/Cross-references: UNIPROT:P13497; GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500C
R/Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A/Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mtld) are encoded
A/Reference number: A58788; MUID:95096114; PMID:7798260
A/Accession: B58788
A/Molecule type: mRNA
A/Residues: 703-986 <TAK>
A/Cross-references: GB:L35279; NID:G619860; PIDN:AAC41710.1; PID:G619861
C/Genetics:
A/Gene: GDB:BMP1; BMP-1
A/Cross-references: GDB:125203; OMIM:112264
A/Map position: 8p21-8p21
C/Function:
A/Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C/Keyword: C/Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g1
F.1-32/Domains: signal sequence #status predicted <SIG>
F.23-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predicted
F.130-321/Domains: astacin homology <AST>
F.322-431/Domains: C1r/C1s repeat homology <C1R1>
F.135-544/Domains: C1r/C1s repeat homology <C1R2>

F:551-587/Domain: EGF homology <EG1>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:707-742/Domain: EGF homology <EG2>
F:747-866/Domain: C1r/C1s repeat homology <C1R4>
F:860-973/Domain: C1r/C1s repeat homology <C1R5>
F:911,142,33,363,599/Binding site: carboxylate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-666/Binding site: zinc (His, His, His, Tyr) #status predicted
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.4%; Score 187.5; DB 1; Length 986;
Best Local Similarity 39.4%; Pred. No. 4.6e-06;
Matches 43; Conservative 18; Mismatches 46; Indels 5; Gaps 3;

	Query Match	9.4%;	Score 187.5;	DB 1;	Length 986;
	.Best Local Similarity	39.4%;	Pred. No. 4.6e-06;		
	Matches	43;	Conservative	18;	Mismatches 43; Indels 5; Gaps 3;
QY	59 KNGVVGSRFPNSYNPRNLLTWRLHSGENTRIQLVFNDGCEGLAEANDICRYDEVED	: :	:	: :	:
Dd	597 KLNGSITSGWEKPEYPNNKCIIQWLVAPTYRISLQPD--FFETEGDNVCXDFVEVYS	: :	:	: :	:
QY	119 ISETSTIIRMGCHKEVPPIKRNRNQIKITERSDDYFPAKKPFKITI	: :	:	: :	:
Dd	654 GTADSKHGKFCG-SSEKPEVIITSQYNMNRVERESDN-TYSKKGFKAIF	: :	:	: :	:

RESULT 8
I19540
procollagen C-endopeptidase (EC 3.4.24.19) precursor, collagen-like splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I19540
R:Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
Dev. Biol. 163, 175-183, 1994
A:Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel
A:Reference number: I19540; MUID:94229342; PMID:8147772
A:Accession: I19540
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Cross-references: 1-991 <RES>
A:Cross-references: UNIPROT:P98063; GB:L24755; NID:g439606; PIDN:AAA17306.1; PID:g439607
C:Genetics: 1
A:Gene: Bmp-1
C:Superfamily: procollagen C-endopeptidase; ascracin homology; C1r/C1s repeat homology; F
C:Keywords: hydrolase; metalloproteinase; zinc
F:135-326/Domain: ascracin homology <AST>
F:556-592/Domain: EGF homology <EG1>
F:596-705/Domain: C1r/C1s repeat homology <C1r>
F:712-747/Domain: EGF homology <EG2>
F:218-222, 228, 277/Binding site: zinc (His, His, His, Tyr) #status predicted
F:219/Active site: Glu #status predicted

	Query Match	9.4%;	Score 187.5;	DB 2;	Length 991;
	Best Local Similarity	39.4%;	Pred. No. 4.9e-06;		
	Matches	43;	Conservative 18;	Mismatches 43;	Indels 5; Gaps 3;
QY	59 KONGVQSRRFPSPYSRNLTLTWRLHSGENTRIQLVFDNGFGLAEANDICRYDEVED		:		
Db	602 KLNSGITSFGWPPEXPNNKNCIWLVAFTQYRISLQDF--FFETEGNDVCKDVEVFAS	: :	:		
QY	119 ISETSTIIIGRMGGHKEVPPIKSRNQIKITFKSDSYFAVAKPFKIYY	:	:	:	:
Db	659 GLTADSKLKHGFCG-SSEKPEVITTSOVNMNRAVEFEESDN-TYSSKGEKFATP	: :	:		

RESULT 9
T09456
Intrinsic factor-B12 receptor Cubilin precursor - human
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T09456
R/Kozakrai, R.; Kristiansen, M.; Silahatoglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N
Blood 91, 3593-3600, 1998
AltTitle: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characterization.

A:Reference number: Z16677; MUID:98241400; PMID:9572993
A:Accession: T09456
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-3623 <KO2>
A:Cross-references: UNIPROT:O60494; EMBL:AF034611; NID:G3929528; PIDN:AC082612.1; PID:G3
C:Genetics:
A:Map position: 10p12
C:Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C:Keywords: receptor; vitamin B12 uptake
F.1-24/Domain: signal sequence #status predicted <SIG>
F.25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
E:436-467/Domain: EGF homology <EGF>

Query Match	9.3%	Score 184.5	DB 2	Length 3623
Best Local Similarity	24.3%	Pred. No. 4.4e-05		
Matches 85	Conservative 3	Mismatches 120	Indels 111	Gaps 17

```

QY 56 OVKNKGVSQSRPFNSVPRNLLTMRLRISGENTLOVFDNQFGLKEAKENDICGAYVE 115
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 935 ILTESTGIIQSGCHNVPRHGINCTMHILVQCNHLLHLMFEF-FLHEPHYN-CINDIIE 991
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 116 VEDI-SEFSTIIRGWCQHKVEVPRPKSRTNOIKITFKSDDYFAVKPGKITY----- 167
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 992 YDVTDEPSL---GRYCG-KSIPSLTSGSNLMVFWYTDs-DLAEYEFLLINYEALSAAT 1046
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 168 SLLEDPOCAAASET-----WMESTSSISGVSNVSPSVTPTLIADALDKIAEF 217
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1047 ACLQDYTDLDLGTFSPNPFNNYNNMECI-----YRI-TVRGOLIA----- 1087
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 218 DTVEDLLKFPNSESQEDLENNYLDTPRYGASY-----HDRK----- 255
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1088 -----VHFTNFSLEBAIGNYTTPLERIDGQYKESPLGIIFYGSNLPRTIISHNKLW 1140
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 256 SKVDLRILNDAKRYSCPTPRNYSVNIREELKLANVAFPRCLLQVRGCGNCGCGTWNMRS 315
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1141 LKFKSDQI-DTRSGRSAYWDSSTG-----CGGN----- 1166
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 316 CTCNNGKVIYKHYEVLQEPFGHI-----KRGRAKTMALVDIQLDHNERC 360
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1169 LTTSGGIFLSPNYPMFYHNSSECYMWLXSSHSAFELBEKQFHLHNNPC 1219
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 10

A5 antigen precursor - African clawed frog
 C:Species: *Xenopus laevis* (African clawed frog)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: JH0466; JQ0948
 R:Takegi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
 N:Neuron 7, 295-307, 1991
 A:Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homology
 A:Reference number: JH0466; MUID:91337458; PMID:1908252
 A:Accession: JH0466
 A:Molecule type: mRNA
 A:Residues: 1-927 <TK>
 A:Cross-references: GB:D01067; GB:D01077; NID:g222962; PIDN:BA01260.1; PID:g222963
 A:Experimental sources: tadpole, brain
 A:Note: this protein has motifs homologous to complement components C1r and C1s and to C
 C:Comment: This protein is a neuronal cell surface molecule involved in the neuronal rec
 C:Superfamily: *Xenopus* A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal h
 C:Keyword: duplication; glycoprotein; transmembrane protein
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:122-927/Product: A5 antigen #status predicted <ASA>
 F:127-138/Domain: C1r/C1s repeat homology <C1R>
 F:147-262/Domain: C1r/C1s repeat homology <C1R2>
 F:274-424/Domain: discoidin I amino-terminal homology <DN1>
 F:430-584/Domain: discoidin I amino-terminal homology <DN2>
 F:646-812/Domain: MAM homology <MAM>
 F:861-883/Domain: transmembrane #status predicted <TM>
 F:150,261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status predicted

Best Local Similarity 27.4%; Pred. No. 3.3e-05;
Matches 61; Conservative 35; Mismatches 91; Indels 36; Gaps 9

[illegible]

RESULT 11

```

dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)
;Species: Drosophila melanogaster
;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 09-Jul-2004
;Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
;Accession: A39288
;Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone
;Reference number: A39288; MUID:92034970; PMID:1840509
;Accession: A39288
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-1057 <SH1>
;Cross-references: UNIPROT:P25723; GB:M76976; NID:G157305; PIDN:AAA28491.1; PID:G157305
;Gene: FlyBase:tlid
;Cross-references: FlyBase:FBgn0003719
;Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; Ctr/Cts rep
;Keywords: duplication; hydrolyase; metalloproteinase; zinc
;136-329/Domain: astacin homology <AST>
;332-464/Domain: Ctr/Cts repeat homology <CtR1>
;468-578/Domain: Ctr/Cts repeat homology <CtR2>
;585-620/Domain: EGF homology <EG1>
;624-740/Domain: Ctr/Cts repeat homology <CtR3>
;747-782/Domain: EGF homology <EG2>
;787-896/Domain: Ctr/Cts repeat homology <CtR4>
;900-1013/Domain: Ctr/Cts repeat homology <CtR5>
;121,225-231,280/Binding site: zinc (His, His, Tyr) #status predicted
;222/Active site: Gu #status predicted

```

Query Match	8.8%;	Score 174.5;	DB 1;	Length 1057;
Best Local Similarity	24.2%;	Pred. No. 5.1e-05;		
Matches	84;	Conservative	45;	Mismatches 115;
			Indels	103;
			Gaps	17

```

123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

```

Db 698 -----RLKKIGCYGHELPVNVSEQSILRLFEFYSRDTVQRSGFAKVIDVECSM 749
QY 304 GNGCG-----GTVMNRSCGNSCKTVKKYKHEVLOFEPGHIKRGRAK 345
Db 750 NNGGQHRCRNTFGSYQCSGRNGYTLA-----ENGHNCTETRCK 788

RESULT 12

T08618

intrinsic factor-B12 receptor CUBILIN precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T08618

R.Moestrup, S.K.; Kozyrak, R.; Kristiansen, M.; Kaye, J.H.; Rasmussen, H.H.; Braut, J. Biol. Chem. 273, 5235-5242, 1998

A:Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies

A:Reference number: Z16459; MUID:98148073; PMID:9478979

A:Accession: T08618

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-3623 <MOB>

A:Cross-references: UNIPROT:O70244; EMBL:AF022247; NID:93834379; PIDN:AAC71661.1; PID:93

C:Genetics:

A:Gene: CUBILIN

C:Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology

C:Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane

F:1-20/Domain: signal sequence #status predicted <Sig>

F:21-163/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <Mat>

F:133-164/Domain: EGF homology <EGF>

F:436-467/Domain: EGF homology <EGF>

Query Match

Best Local Similarity 26.4%; Pred. No. 0.00033;

Matches 62; Conservative 35; Mismatches 96; Indels 40; Gaps 10;

QY 15

FSCSDDTSATFQSSASIKALRNANLRDESNHLTDLYRDE---TIQVKGNGVQSPRP 70

Db 890 FCCSNIPSEFITVYNILVYTFVKSSSMENRGFTAKFSSDKLCEGLTASTGIIESPGHP 949

QY 71

NVPYNNLLTWRLHSGENTRIQLVFNQGLEAENDICRYDFVEEDISFTIIRGM 130

Db 950 NVPYGVNCTWVHVVRGQLRLER-SSFLYLFHYN--CTNYLLELYDTAQTFL--GRY 1004

QY 131

CGHKEVPPRIKSRTOIKITFKSDDYFVAKPGFKIYVSLLEDFOAPAAS----- 179

Db 1005 CG-KKIPSLTNSNSIKILFVSDS-ALAHGFSINYEAD-----ASSVCLYDTDNG 1057

QY 180

-----ETNWSVTSSISGVSYN-SPSVTDTPLADALDKKIAEFTVED 222

Db 1058 MLSPNFPNNYSNWEICIRITVGLNQIALHFTDFTL-EDYFGSCVDVFEIRD 1111

RESULT 13

JCT629

membrane-type frizzled-related protein - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C:Accession: JCT629

R.Katch, M.

Biochem. Biophys. Res. Commun. 282, 116-123, 2001

A:Title: Molecular cloning and characterization of MRP, a novel gene encoding a membra

A:Reference number: JCT629; MUID:21164708; PMID:11263980

A:Accession: JCT629

A:Molecule type: mRNA

A:Residues: 1-579 <KAT>

A:Cross-references: UNIPROT:Q9BY79; DBJ:AB055505

C:Comment: This protein, which plays key roles in medulla oblongata as a regulator of th

ubulin domains.

C:Genetics:

A:Gene: mfrp

A:Map position: 11q23

C:Keywords: transmembrane protein

Query Match 8.1%; Score 161; DB 2; Length 579;

Best Local Similarity 26.2%; Pred. No. 0.00024;

Matches 49; Conservative 29; Mismatches 63; Indels 46; Gaps 9;

QY 11

ICANFCGRDTSATFQSSASIKALRNANLRDESN-----HLDLYRDEFTIYKVG 60

Db 278

VCDGFANCADS-----DETNSAKFSGCGGNLTGL----- 308

QY 61

NGVQSPRPNSYPNNLLTWRLHSGENTRIQLVFNQGLEAENDICRYDFVEEDIS 120

Db 309

OCTESTPSYLOQYPRQLCTWHISVPAGHSIELOPHN-FSLF--AQDECKDPYEVYETS 365

QY 121

ETSTI-IRGRWCGHKEVPRIKSRTOIKITFKSDDYFVAKPGFKIYVSLLEDFO-PA 178

Db 366

SSGARSLGRFCG-AEPPHLVSSHLEAVLERT-DHGISGGSFATYLAFAFNATENPCGP 423

QY 179

SETNWS 185

Db 424

SELSCOA 430

RESULT 14

T30337

polyprotein - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C:Accession: T30337

R.Yang, J.C.; Lindsey, L.L.; Hedrick, J.L.

submitted to the EMBL Data Library, March 1998

A:Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from Xe

A:Reference number: Z20829

A:Accession: T30337

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1524 <YAN>

A:Cross-references: UNIPROT:Q91574; EMBL:U81290; NID:92981640; PID:92981641; PIDN:AAC247

C:Superfamily: trypsin related polypeptide; trypsin homology

Query Match

Best Local Similarity 7.8%; Score 156.5; DB 2; Length 1524;

Matches 54; Conservative 36; Mismatches 72; Indels 45; Gaps 10;

QY 58

VKNGVQSPRPNSYPNNLLTWRLHSGENTRIQLVFNQGLEAENDICRYDFVEE 117

Db 425

LKKKMIVSPNVPDPYPRKTCSTWIEAPENHIVKLPED-FNVEYGHG--CIYDAVEY 491

QY 118

DISETSTIIRGRWCGHKEVPRIKSRTOIKITFKSD--DYFVAKPGFKI----- 165

Db 492

DGAERKOLI-ARLCGY-TLPLPISSPENTMLIRFKTDMENSY---PGKVFQSFVPEK 545

QY 166

YSLLEDFOPAASSETNWSVTSSISGVSYNSPSVTDPLIADALDKKIAEFTVEDL 225

Db 546

QPSLPVDTP-TISLHLRAIALDYCGMAPMTPKMWLRIVCG-----E 588

QY 226

YFPESWQEDLENNYLDTPRYGRSYH 252

Db 589

EASPSWMPVOQIFPL-----RTFH 608

RESULT 15

S58984

development protein tolkin (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: S58984

R.Fineili, A.L.; Xie, T.; Boessie, C.A.; Blackman, R.K.; Padgett, R.W.

Genetics 141, 271-281, 1995

A:Title: The tolkin gene is a tollid/BMP-1 homologue that is essential for Drosophila c

A:Reference number: S58984; MUID:96042912; PMID:8536976

A:Accession: S58984

A:Molecule type: mRNA

A:Residues: 1-1464 <FTN>

A:Cross-references: UNIPROT:O24132; EMBL:U34777; NID:91002985; PIDN:AAC47015.1; PID:9100

A/Note: the authors did not translate the codon for residue 722

C/Genetics:

A/Gene: tolkin

A/Cross-references: FlyBase:FBgn004885

C/Keywords: hydrolase; metalloproteinase; zinc

F/529-722/Domain: aetacin homology <AST>

F/958-993/Domain: EGF homology <EGF>

F/118-1153/Domain: EGF homology <EGF>

F/614-618-624/Binding site: zinc (His, His, Tyr) #status predicted

F/615/Active site: Glu #status predicted

Query Match

Best Local Similarity 7.4%; Score 153; DB 2; Length 1464;

Matches 57; Conservative 27; Mismatches 60; Indels 86; Gaps 9;

5 IFPTLTICAN-----FCSCRTSATPQASIKALRNANLRDESNHLDLYRDETQ 57

1059 VTYYSKLGKGNRLKRICTFCG-----SSIPPTAT-----SESVALRLEFHSKSIQ 1103

58 VKG-----NGY-----63

1104 RSGFAVFPFDIDECANVNGCGHBCRNITGSIYICMCHNGYSMHENGHCKECKEYS 1163

64 -----VQSPRPSPNSPRNLLTWRLHSEONTRIQLVFDNQGLEAENDICRYDFVEED 118

1164 APFGTIFSPVDPDYPNADCVWHFITTPGHRILKIF--NEFDVSHQE--CTYDNVAVYD 1220

119 ISETSTIIRGMCQKHEVPRIKSRNQIKITKSDDYFAKQGFKIYIS 168

1221 GSESSSVLGRFCGDK-IPPISTSTSNQMYVWLKTDKN-KQKNGFTASHS 1268

Db

Query

119 ISETSTIIRGMCQKHEVPRIKSRNQIKITKSDDYFAKQGFKIYIS 168

1221 GSESSSVLGRFCGDK-IPPISTSTSNQMYVWLKTDKN-KQKNGFTASHS 1268

Db

Query Match

Best Local Similarity 7.4%; Score 149; DB 2; Length 1070;

Matches 43; Conservative 34; Mismatches 66; Indels 10; Gaps 7;

61 NGVQSPRPNSPRNLLTWRLHSEONTRIQLVFDNQGLEAENDICRYDFVEEDIS 120

683 SGTISPSFEDLPPDKNCVWHISAKRGHTLVNFTTHMD--LEWRDECDLDPVRYTAVV 740

121 ETSITIRGMCQKHEVPRIKSRNQIKITKSDDYFAKQGFKIYISLEDEPOAAASE 180

741 GNKERLOGQYCGFM-APPSITSLNELRIEFRSDD-TLQKTGFSMDY--VADVDECASSN 796

181 TNWESVTSISGVSYSPTDPTLADALDKK 213

797 GGCKHICENTVG-SFHC-SCREGFTLAD--DEK 825

Db

Query

181 TNWESVTSISGVSYSPTDPTLADALDKK 213

797 GGCKHICENTVG-SFHC-SCREGFTLAD--DEK 825

Db

Query Match

Best Local Similarity 7.4%; Score 149; DB 2; Length 1070;

Matches 43; Conservative 34; Mismatches 66; Indels 10; Gaps 7;

61 NGVQSPRPNSPRNLLTWRLHSEONTRIQLVFDNQGLEAENDICRYDFVEEDIS 120

683 SGTISPSFEDLPPDKNCVWHISAKRGHTLVNFTTHMD--LEWRDECDLDPVRYTAVV 740

121 ETSITIRGMCQKHEVPRIKSRNQIKITKSDDYFAKQGFKIYISLEDEPOAAASE 180

741 GNKERLOGQYCGFM-APPSITSLNELRIEFRSDD-TLQKTGFSMDY--VADVDECASSN 796

181 TNWESVTSISGVSYSPTDPTLADALDKK 213

797 GGCKHICENTVG-SFHC-SCREGFTLAD--DEK 825

Db

Query

181 TNWESVTSISGVSYSPTDPTLADALDKK 213

797 GGCKHICENTVG-SFHC-SCREGFTLAD--DEK 825

Db

Query Match

Best Local Similarity 7.4%; Score 149; DB 2; Length 1070;

Matches 43; Conservative 34; Mismatches 66; Indels 10; Gaps 7;

61 NGVQSPRPNSPRNLLTWRLHSEONTRIQLVFDNQGLEAENDICRYDFVEEDIS 120

683 SGTISPSFEDLPPDKNCVWHISAKRGHTLVNFTTHMD--LEWRDECDLDPVRYTAVV 740

121 ETSITIRGMCQKHEVPRIKSRNQIKITKSDDYFAKQGFKIYISLEDEPOAAASE 180

741 GNKERLOGQYCGFM-APPSITSLNELRIEFRSDD-TLQKTGFSMDY--VADVDECASSN 796

181 TNWESVTSISGVSYSPTDPTLADALDKK 213

797 GGCKHICENTVG-SFHC-SCREGFTLAD--DEK 825

Db

Query

181 TNWESVTSISGVSYSPTDPTLADALDKK 213

797 GGCKHICENTVG-SFHC-SCREGFTLAD--DEK 825

Db

C/Accession: A59271

R/Title: S.; Vornpu-Jensen, T.; Stover, C.M.; Schwaebble, W.J.; Laursen, S.B.; Poulsen, K

Nature 386, 506-510, 1997

A/Title: A second serine protease associated with mannan-binding lectin that activates

A/Reference number: A59271; PMID:97242412; PMID:9087411

A/Accession: A59271

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-686 <JEN>

A/Cross-references: UNIPROT:O00187; GB:Y09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007

A/Experimental source: tissue liver

A/Note: Submitted to GenBank, December 1996

A/Note: parts of this sequence, including the amino end of the mature protein, were det

C/Genetics:

A/Gene: GDB:MASP2

A/Cross-references: GDB:6071500

A/Map position: 1p36.2-1p36.3

C/Suprafamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homo

C/Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine

F/1-15/Domain: signal sequence #status predicted <SIG>

F/16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MNT>

F/19-134/Domain: C1r/C1s repeat homology <C1R1>

F/142-180/Domain: EGF homology <EGF>

F/184-293/Domain: complement factor H repeat homology <C1R2>

F/300-361/Domain: complement factor H repeat homology <FH1>

F/366-430/Domain: complement factor H repeat homology <FH2>

F/445-679/Domain: trypsin homology <TRY>

F/72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552

F/158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

F/444-445/Cleavage site: Arg-11e (autolytic) #status predicted

F/483,532,633/Active site: His, Asp, Ser #status predicted

Query Match

Best Local Similarity 7.4%; Score 148; DB 1; Length 686;

Matches 80; Conservative 54; Mismatches 134; Indels 158; Gaps 17;

12 CAN-----FCSCRTSATPQASIKALRNANLRDESNHLDLYRDET-----IQV 58

156 CHNHGFGFCSC-----AGY--LHRKRTCSALCSGOVET 190

59 KGVQSPRPNSPRNLLTWRLHSEONTRIQLVFDNQGLEAENDICRYDFVEED 118

191 QRGELSPSEYPRPYKLSCTYSISLEGFSVILDFVESFVETHPELCPYDFUKIQT 250

119 ISETSTIIRGMCQKHEVPRIKSRNQIKITKSD-----155

251 DREB-----HGFPCG-KTLPHRIETKSNVTYITFVDESGDHGCMKIHYSTAHACEYMA 305

156 -----YVAKRGFKIY-----YSLE-----DEPOAAASETNMESVTSISGV 194

306 PRNGHVSPOAKIILKDSIFETGYELLQGLPLKSTFVAVQCKGSDRPPACSIYD 365

195 YNSPVTDPTLADALDKIAE-----DYEDLLKYENPESMOEDLENMYLDTPRYRG 248

366 CGRP-----DLPGRVEXEYITPGVTVYAVAIQY-----SCEETPYTM-----403

249 RSTHDKSKVLDRLNDDAKRSCTPRNRSVNRBELKLANVFFPRCLLVOR-----301

404 -----KXNDG--KYVCADGFWTSSGKESLP--VCEVCGISATFTGRLY 446

302 -----CGNGCGGV-----NMRSCNCSGTVKRYHEVLOFEGHILKRG 342

447 GGGKAKPGDPFQVQVLLGGTTAGALLYDNNVLTAAHAYVEQGHDSALDIRNGTILKRLS 506

343 RAKTMA 348

507 PHYTOA 512

Db

Query

343 RAKTMA 348

507 PHYTOA 512

Db

Query Match

Best Local Similarity 7.4%; Score 148; DB 1; Length 686;

Matches 80; Conservative 54; Mismatches 134; Indels 158; Gaps 17;

12 CAN-----FCSCRTSATPQASIKALRNANLRDESNHLDLYRDET-----IQV 58

156 CHNHGFGFCSC-----AGY--LHRKRTCSALCSGOVET 190

59 KGVQSPRPNSPRNLLTWRLHSEONTRIQLVFDNQGLEAENDICRYDFVEED 118

191 QRGELSPSEYPRPYKLSCTYSISLEGFSVILDFVESFVETHPELCPYDFUKIQT 250

119 ISETSTIIRGMCQKHEVPRIKSRNQIKITKSD-----155

251 DREB-----HGFPCG-KTLPHRIETKSNVTYITFVDESGDHGCMKIHYSTAHACEYMA 305

156 -----YVAKRGFKIY-----YSLE-----DEPOAAASETNMESVTSISGV 194

306 PRNGHVSPOAKIILKDSIFETGYELLQGLPLKSTFVAVQCKGSDRPPACSIYD 365

195 YNSPVTDPTLADALDKIAE-----DYEDLLKYENPESMOEDLENMYLDTPRYRG 248

366 CGRP-----DLPGRVEXEYITPGVTVYAVAIQY-----SCEETPYTM-----403

249 RSTHDKSKVLDRLNDDAKRSCTPRNRSVNRBELKLANVFFPRCLLVOR-----301

404 -----KXNDG--KYVCADGFWTSSGKESLP--VCEVCGISATFTGRLY 446

302 -----CGNGCGGV-----NMRSCNCSGTVKRYHEVLOFEGHILKRG 342

447 GGGKAKPGDPFQVQVLLGGTTAGALLYDNNVLTAAHAYVEQGHDSALDIRNGTILKRLS 506

343 RAKTMA 348

507 PHYTOA 512

Db

Query

343 RAKTMA 348

507 PHYTOA 512

Db

Query Match

Best Local Similarity 7.4%; Score 148; DB 1; Length 686;

Matches 80; Conservative 54; Mismatches 134; Indels 158; Gaps 17;

12 CAN-----FCSCRTSATPQASIKALRNANLRDESNHLDLYRDET-----IQV 58

156 CHNHGFGFCSC-----AGY--LHRKRTCSALCSGOVET 190

59 KGVQSPRPNSPRNLLTWRLHSEONTRIQLVFDNQGLEAENDICRYDFVEED 118

191 QRGELSPSEYPRPYKLSCTYSISLEGFSVILDFVESFVETHPELCPYDFUKIQT 250

119 ISETSTIIRGMCQKHEVPRIKSRNQIKITKSD-----155

251 DREB-----HGFPCG-KTLPHRIETKSNVTYITFVDESGDHGCMKIHYSTAHACEYMA 305

156 -----YVAKRGFKIY-----YSLE-----DEPOAAASETNMESVTSISGV 194

306 PRNGHVSPOAKIILKDSIFETGYELLQGLPLKSTFVAVQCKGSDRPPACSIYD 365

195 YNSPVTDPTLADALDKIAE-----DYEDLLKYENPESMOEDLENMYLDTPRYRG 248

366 CGRP-----DLPGRVEXEYITPGVTVYAVAIQY-----SCEETPYTM-----403

249 RSTHDKSKVLDRLNDDAKRSCTPRNRSVNRBELKLANVFFPRCLLVOR-----301

404 -----KXNDG--KYVCADGFWTSSGKESLP--VCEVCGISATFTGRLY 446

302 -----CGNGCGGV-----NMRSCNCSGTVKRYHEVLOFEGHILKRG 342

447 GGGKAKPGDPFQVQVLLGGTTAGALLYDNNVLTAAHAYVEQGHDSALDIRNGTILKRLS 506

343 RAKTMA 348

507 PHYTOA 512

Db

Query

343 RAKTMA 348

507 PHYTOA 512

Db

Query Match

Best Local Similarity 7.4%; Score 148; DB 1; Length 686;

Matches 80; Conservative 54; Mismatches 134; Indels 158; Gaps 17;

12 CAN-----FCSCRTSATPQASIKALRNANLRDESNHLDLYRDET-----IQV 58

156 CHNHGFGFCSC-----AGY--LHRKRTCSALCSGOVET 190

59 KGVQSPRPNSPRNLLTWRLHSEONTRIQLVFDNQGLEAENDICRYDFVEED 118

191 QRGELSPSEYPRPYKLSCTYSISLEGFSVILDFVESFVETHPELCPYDFUKIQT 250

119 ISETSTIIRGMCQKHEVPRIKSRNQIKITKSD-----155

251 DREB-----HGFPCG-KTLPHRIETKSNVTYITFVDESGDHGCMKIHYSTAHACEYMA 305

156 -----YVAKRGFKIY-----YSLE-----DEPOAAASETNMESVTSISGV 194

306 PRNGHVSPOAKIILKDSIFETGYELLQGLPLKSTFVAVQCKGSDRPPACSIYD 365

195 YNSPVTDPTLADALDKIAE-----DYEDLLKYENPESMOEDLENMYLDTPRYRG 248

366 CGRP-----DLPGRVEXEYITPGVTVYAVAIQY-----SCEETPYTM-----403

249 RSTHDKSKVLDRLNDDAKRSCTPRNRSVNRBELKLANVFFPRCLLVOR-----301

404 -----KXNDG--KYVCADGFWTSSGKESLP--VCEVCGISATFTGRLY 446

302 -----CGNGCGGV-----NMRSCNCSGTVKRYHEVLOFEGHILKRG 342

447 GGGKAKPGDPFQVQVLLGGTTAGALLYDNNVLTAAHAYVEQGHDSALDIRNGTILKRLS 506

343 RAKTMA 348

507 PHYTOA 512

Db

Query

343 RAKTMA 348

507 PHYTOA 512

Db

Query Match

Best Local Similarity 7.4%; Score 148; DB 1; Length 686;

Matches 80; Conservative 54; Mismatches 134; Indels 158; Gaps 17;

12 CAN-----FCSCRTSATPQASIKALRNANLRDESNHLDLYRDET-----IQV 58

156 CHNHGFGFCSC-----AGY--LHRKRTCSALCSGOVET 190

59 KGVQSPRPNSPRNLLTWRLHSEONTRIQLVFDNQGLEAENDICRYDFVEED 118

191 QRGELSPSEYPRPYKLSCTYSISLEGFSVILDFVESFVETHPELCPYDFUKIQT 250

119 ISETSTIIRGMCQKHEVPRIKSRNQIKITKSD-----155

251 DREB-----HGFPCG-KTLPHRIETKSNVTYITFVDESGDHGCMKIHYSTAHACEYMA 305

156 -----YVAKRGFKIY-----YSLE-----DEPOAAASETNMESVTSISGV 194

306 PRNGHVSPOAKIILKDSIFETGYELLQGLPLKSTFVAVQCKGSDRPPACSIYD 365

195 YNSPVTDPTLADALDKIAE-----DYEDLLKYENPESMOEDLENMYLDTPRYRG 248

366 CGRP-----DLPGRVEXEYITPGVTVYAVAIQY-----SCEETPYTM-----403

249 RSTHDKSKVLDRLNDDAKRSCTPRNRSVNRBELKLANVFFPRCLLVOR-----301

404 -----KXNDG--KYVCADGFWTSSGKESLP--VCEVCGISATFTGRLY 446

302 -----CGNGCGGV-----NMRSCNCSGTVKRYHEVLOFEGHILKRG 342

447 GGGKAKPGDPFQVQVLLGGTTAGALLYDNNVLTAAHAYVEQGHDSALDIRNGTILKRLS 506

343 RAKTMA 348

507 PHYTOA 512

Db

Query

343 RAKTMA 348

507 PHYTOA 512

Db

Query Match

Best Local Similarity 7.4%; Score 148; DB 1; Length 686;

Matches 80; Conservative 54; Mismatches 134; Indels 158; Gaps 17;

12 CAN-----FCSCRTSATPQASIKALRNANLRDESNHLDLYRDET-----IQV 58

156 CHNHGFGFCSC-----AGY--LHRKRTCSALCSGOVET 190

59 KGVQSPRPNSPRNLLTWRLHSEONTRIQLVFDNQGLEAENDICRYDFVEED 118

C:Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 09-Jul-2004
C:Accession: A59386
R:Ranko, S.
submitted to the Protein Sequence Database, March 2001
A:Reference number: A59386
A:Accession: A59386
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-2403 <SAN>
A:Cross-references: UNIPROT:Q9UGM2

Query Match 7.2%; Score 144; DB 2; Length 2403;
Best Local Similarity 22.0%; Pred. No. 0.03;
Matches 72; Conservative 49; Mismatches 112; Indels 94; Gaps 16;

35 NANLRD-----ESNHLT-----DLRRDETQVKG-----NGVQSPRPNSYPRNLL 78
1964 NQNRHEDAGVTCGNHLSPPAPPLITRPNNTDYS CGGLSQSPSGDPSSPFYGNYPNNAK 2023
QY 79 LTRWLRHSCENTRIQLVFNQGLEAENDI-----CRYDFVEVEDISESTIRGRMCGH 133
DB 2024 CWMDELVQNNYVATYIF-----RVQLEGCGNYIIEVFDGPRYSSPLIARVCDG 2073
QY 134 KEVPRIRSRNQIKITFKSDDYFVAKPGFKI-YYS-----LLEDQPPAAASETN 182
DB 2074 AR--GSFTSSNFMGIRFIS-DHSITRRGFRAYEYSSPNDSTNLLCLPNHQASVSRBY 2130
QY 183 WES-----VTSSISGVSYNSPVTDTLTALADLDR-----KLAEPDYB----- 221
DB 2131 LOSLFRSASDLVISTWNGYEGCRPQIT-PNLVITFTIPYSGCGTFKQADNDTIDYSNFLTA 2189
QY 222 -----DLKYPNESPQWQEDLENNYLDTPPRYGRSYHDKRSKYLDRL--NDDA 267
DB 2190 AVSGGIKRRTDRLRHVSGRM---LQNTWVDTWYIANDTHIVANTIOVEEVQGNPVD 2245
QY 268 K-----RYSCTPRNYSVNIREE 285
DB 2246 NISFYTSSGFLYPVTSPRYVDLNDL 2272

RESULT 19
154763
Ra-reactive factor (EC 3.4.21.-) 1 precursor - human
N:Alternate names: mannose binding protein-associated serine proteinase 1 (MASP-1)
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: I54763; JN0883
R:Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.
Int. Immunol. 6, 665-669, 1994
A:Title: Molecular characterization of a novel serine protease involved in activation of
A:Reference number: I54763; MUID:94289349; PMID:8018603
A:Accession: I54763
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-699 <SAT>
A:Cross-references: UNIPROT:P48740; GB:D28593; NID:G790963; PIDN:BAA05928.1; PID:G471128
R:Takada, F.; Takayama, Y.; Hattuse, H.; Kawakami, M.
Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A:Title: A new member of the C1s family of complement proteins found in a bactericidal F
A:Reference number: JN0883; MUID:94059062; PMID:8240317
A:Accession: JN0883
A:Molecule type: mRNA
A:Residues: 1-224,'E',236-284,'G',286-498,'K',500-542,'K',544-642,'S',644-699 <TAK>
A:Cross-references: DDBJ:D17525; NID:G439712; PIDN:BAA04477.1; PID:G439713
A:Experimental source: liver
C:Comment: This is a serum bactericidal factor that activates complement C4 and C2 compo
C:Genetics:
A:Gene: GDB:MASP1; GDB:CRARF; CRARF1; PRSS5; MASP
A:Cross-references: GDB:361104; GDB:330954; OMIM:600521
A:Map position: 3q27-3q28
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; hydro
F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-448,449-699/Product: Ra-reactive factor #status predicted <MAT>
F:19-135/Domain: C1r/C1s repeat homology <C1r1>
F:143-181/Domain: EGF homology <EGF>
F:185-294/Domain: C1r/C1s repeat homology <C1R2>
F:301-362/Domain: complement factor H repeat homology <FH1>
F:367-432/Domain: complement factor H repeat homology <FH2>
F:449-691/Domain: trypsin homology <TRY>
F:49,178,407/Binding site: carbohydrate (asn) (covalent) #status predicted
F:73-91,143-157,153-166,168-181,185-212,242-260,301-349,329-362,367-414,397-432,436-572,
F:159/Modified site: erythro-beta-hydroxyasparagine (asn) #status predicted
F:448-449/Cleavage site: Arg-Ile (autolytic) #status predicted
F:490,552,646/Active site: His, Asp, Ser #status predicted

Query Match 7.2%; Score 143; DB 1; Length 699;
Best Local Similarity 19.5%; Pred. No. 0.0071;
Matches 67; Conservative 52; Mismatches 11; Indels 108; Gaps 14;

6 FVYTLICANFGSCDRTPASATPQASIKALRNANLRDESNHLLDLYRRDETQVKGNGVQ 65
156 YCHNVIIGYVYCSR-----FGYLIHDTNRTCRVCCSDNLF-----TQRTGVIT 198
QY 66 SPRPNNSYPRNLLLTRWLRHSCENTRIQLVFNQGLEAENDICRYDFVEVEDISESTI 125
DB 199 SPDFNPYPKSECLYTLLEEGFMWNLQFEDIFDIQHPVPCPYDYTKI---KVGPK 254
QY 126 IRGRWCGHKEVPRIRSRNQIKITFKSD--DPPAAASETWSVTSISGVSYNSPVT 155
DB 225 VLGRPCGKR-APEPSTGSHVLILFHSDNAENRGWRLSYRAGNECPLOPVHGKIE 313
QY 156 ----YEV-----AKGFKIYVSLLE--DPPAAASETWSVTSISGVSYNSPVT 201
DB 314 PSQAKYFFKQDVLVSCDGYKVLKDNVEMDFQIECLKDGTWSNKPICKIIVDCRAPGEL 373
QY 202 DPTLIADLDDKIAEFVIEDLKYFNPSQWQEDLENNYLDTPPRYGRSYHDKRSKYLDL 261
DB 374 EHGILTFSTRNLT--LYKSEIKI---SCQE-----PYKK----- 403
QY 262 RLNDDAKRYSCTPRNSYVN--IREELKLVANVFFPRCLLVORCG 303
DB 404 MLNNNTGTGYTCSAQGVMMNKKVLGRSL-----PTCLPV--CG 437

RESULT 20
730018
Hypothetical protein F38B9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30018
R:Wu, X.; Gatlung, S.
submitted to the EMBL Data Library, January 1996
A:Description: The sequence of C. elegans cosmid F38B9.
A:Reference number: Z20722
A:Accession: T30018
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-767 <WUX>
A:Cross-references: UNIPROT:Q20176; EMBL:U46668; PIDN:AAA93348.1; CESP:F38B9.2
C:Genetics:
A:Gene: CESP:F38B9.2
A:Introns: 13/1; 37/3; 62/1; 89/1; 127/1; 164/2; 182/1; 235/3; 269/3; 321/2; 360/1; 455/
Query Match 7.1%; Score 141.5; DB 2; Length 767;
Best Local Similarity 24.7%; Pred. No. 0.01;
Matches 77; Conservative 44; Mismatches 114; Indels 77; Gaps 19;

QY 62 GYVQSPRPNSYPRNLLLTRWLRHSCENTRIQLVFNQGLEAENDICRYD-FVEVEDIS 120
DB 232 GVHSPPKYPSEYPPSDCOMTIIHVDENSOVAIEF-VYFHLBOHKE--CIYRLILTFGIS 288
QY 121 ETS----TIIRGRWCGHKEVPRIRSRNQIKITFKSDDYFVAKPGFKIYVSLLEDQPA 176
DB 289 KNSKDKGKEMSEITFGILIE-KTIVSKTNQISLRPFSN-SVQKTGFLRFT--KELNEC 344

```

Qy 177 AASE-----TNWESYTSISGV-----SYNSPVTPTL 205
Db 345 ATDKNICHHYCVTVGGFKACRVGYSLSNGFSCDSTCGYIKASNGSISPNPPEMYP 404
Qy 206 IADALDKKIAEFDTVEDLLKY--FNPSWQEDLENNYL--DTPRYGRSYHDKRSKVDL 260
Db 405 NSKTCIMEIEAPDGYHIFLNFTEKFNVEGMKTECAVDYVKIGSEKLCG-EYH-----455
Qy 261 DRUNDQKRYSCTPRYSVNIREELKLVNV---FPRCLL-VORC-GGNCCG-----G 309
Db 456 ----EALLFT-TPRN--RVRIEFSSDSSVERDGFANFIADFDQNDNAGCEHTQW 506
Qy 310 TVNMRSCTCNSG 321
Db 507 RLGSYVCTCNPG 518

```

Search completed: November 10, 2005, 09:36:10
 Job time : 43.0683 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:21:06 / Search time 166.998 Seconds
(without alignments)
1134.561 Million cell updates/sec

Title: US-10-606-055-2
Perfect score: 1994
Sequence: 1 MRLRLVYTLICANFCSCRD.....DIQLDHERDCICSGRPPR 370

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database: Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1994	100.0	370	2	Q9GZP0
2	1949	97.7	364	2	Q9BWS5
3	1775	89.0	370	2	Q9EOT1
4	1737	87.1	370	2	Q9ZS17
5	1493	74.9	300	2	Q6V9H4
6	1141	57.2	261	2	Q8K2L3
7	753	37.8	345	2	Q91946
8	752	37.7	345	2	Q9QY71
9	750	37.6	345	2	Q8CT19
10	744	37.3	345	2	Q9E0X6
11	742.5	37.2	345	2	Q9UL22
12	742	37.2	345	2	Q9JHV8
13	741.5	37.2	345	2	Q8NRA1
14	632	31.7	258	2	Q8K429
15	189.5	9.5	707	1	BMP1_XENTLA
16	189.5	9.5	977	2	Q91925
17	188.5	9.5	735	2	Q57381
18	188.5	9.5	735	2	Q66K13
19	188.5	9.5	1007	2	Q8J128
20	187.5	9.4	241	2	Q9Z135
21	187.5	9.4	725	2	Q6P550
22	187.5	9.4	966	1	BMP1_HUMAN
23	187.5	9.4	991	1	BMP1_MOUSE
24	187.5	9.4	991	2	Q6N2M2
25	186.5	9.4	1015	2	Q9Y6L7
26	186.5	9.4	1078	2	Q9U000
27	184.5	9.3	3494	2	Q7LC53
28	184.5	9.3	3623	2	Q60494
29	183.5	9.2	1012	2	Q9WVW6
30	180.5	9.1	1022	1	TLD_BRARE
31	177	8.9	954	2	Q75UQ6

32	176	8.8	928	1	NRPI_XENTLA	P28824 xenopus lae
33	175.5	8.8	309	2	Q6T455	Q6T495 brachydanio
34	175.5	8.8	3620	2	Q9RT53	Q9RT53 canis famli
35	175	8.8	871	2	Q6T869	Q6T869 brachydanio
36	175	8.8	959	2	Q69DB7	Q69DB7 brachydanio
37	175	8.8	959	2	Q6RT22	Q6RT22 brachydanio
38	175	8.8	959	2	Q6RT70	Q6RT70 brachydanio
39	174.5	8.8	808	2	Q7YU36	Q7YU36 drosophila
40	174.5	8.8	1019	2	Q57382	Q57382 xenopus lae
41	174.5	8.8	1067	1	TLD_DROME	P25723 drosophila
42	173.5	8.7	691	2	Q57658	Q57658 gallus gall
43	173.5	8.7	1008	2	Q9DER7	Q9DER7 gallus gall
44	173	8.7	3623	2	Q70244	Q70244 rattus norv
45	172.5	8.7	1013	2	Q43897	Q43897 homo sapien
46	172.5	8.7	1013	2	Q9N0S4	Q9N0S4 homo sapien
47	171.5	8.6	538	2	Q6AM49	Q6AM49 homo sapien
48	171.5	8.6	609	2	Q96190	Q96190 homo sapien
49	171.5	8.6	641	2	Q7LSW6	Q7LSW6 homo sapien
50	171.5	8.6	644	2	Q961H5	Q961H5 homo sapien
51	171.5	8.6	704	2	Q9H2E1	Q9H2E1 homo sapien
52	171.5	8.6	906	2	Q6X907	Q6X907 homo sapien
53	171.5	8.6	923	1	NRPI_HUMAN	Q14786 homo sapien
54	171.5	8.6	923	2	Q86T59	Q86T59 homo sapien
55	170.5	8.6	923	2	Q6BDN3	Q6BDN3 homo sapien
56	170.5	8.5	913	2	Q6NUE0	Q6NUE0 xenopus lae
57	169.5	8.5	746	2	Q8IAD8	Q8IAD8 halocynthia
58	168	8.4	923	1	NRPI_CHICK	P79795 gallus gall
59	168	8.4	923	2	Q6PAR3	Q6PAR3 mus musculu
60	167.5	8.4	3670	1	CSMO14	Q72407 homo sapien
61	167	8.4	905	2	Q800L4	Q800L4 gallus gall
62	167	8.4	919	2	Q8UVR0	Q8UVR0 gallus gall
63	167	8.4	921	2	Q9OX38	Q9OX38 rattus norv
64	167	8.4	922	1	NRPI_RAT	Q9WJ99 rattus norv
65	167	8.4	936	2	Q8UVQ9	Q8UVQ9 gallus gall
66	166.5	8.4	574	2	Q86RL8	Q86RL8 illyanassa o
67	166.5	8.4	923	1	NRPI_BRARE	Q8GKX6 brachydanio
68	166.5	8.4	923	2	Q69DB8	Q69DB8 brachydanio
69	166.5	8.4	1013	2	Q62381	Q62381 mus musculu
70	164.5	8.2	746	2	Q01654	Q01654 halocynthia
71	164	8.2	923	1	NRPI_MOUSE	P97333 mus musculu
72	163.5	8.2	927	2	Q6T490	Q6T490 brachydanio
73	163.5	8.2	927	2	Q6T868	Q6T868 brachydanio
74	162	8.1	579	2	Q96DQ9	Q96DQ9 homo sapien
75	161	8.1	579	2	Q9BBY9	Q9BBY9 homo sapien
76	160.5	8.0	927	2	Q69DB6	Q69DB6 brachydanio
77	159.5	8.0	677	2	Q9VYC7	Q9VYC7 drosophila
78	159	8.0	555	2	Q9H2E2	Q9H2E2 homo sapien
79	159	8.0	733	2	Q9Z0S0	Q9Z0S0 mus musculu
80	159	8.0	733	2	Q8CD27	Q8CD27 mus musculu
81	159	8.0	901	2	Q9H2D5	Q9H2D5 homo sapien
82	159	8.0	901	2	Q9H2E4	Q9H2E4 homo sapien
83	159	8.0	906	2	Q9H2D4	Q9H2D4 homo sapien
84	159	8.0	906	2	Q9H2E3	Q9H2E3 homo sapien
85	159	8.0	931	1	NRPI_HUMAN	Q60462 homo sapien
86	159	8.0	931	2	Q7Z3T9	Q7Z3T9 homo sapien
87	158	7.9	578	2	Q8BPP4	Q8BPP4 mus musculu
88	157	7.9	145	2	Q8BPP0	Q8BPP0 mus musculu
89	157	7.9	925	1	NRPI_RAT	Q35276 rattus norv
90	157	7.9	926	2	Q8Q2Y7	Q8Q2Y7 mus musculu
91	157	7.9	931	1	NRPI_MOUSE	Q53715 mus musculu
92	156.5	7.8	860	2	Q7QAH1	Q7QAH1 anopheles g
93	156.5	7.8	936	2	Q8IFX2	Q8IFX2 ciassospora
94	156.5	7.8	1524	2	Q91674	Q91674 xenopus lae
95	155	7.8	584	2	Q8K480	Q8K480 mus musculu
96	155	7.8	697	2	Q8CG43	Q8CG43 rattus norv
97	154.5	7.7	951	2	Q20176	Q20176 caenorhabdl
98	153	7.7	449	2	Q9SRA3	Q9SRA3 drosophila
99	153	7.7	701	2	Q9JUS9	Q9JUS9 rattus norv
100	153	7.7	1464	2	Q23995	Q23995 drosophila

ALIGNMENTS

```

RESULT 1
O9GZPO PRELIMINARY: PRT: 370 AA.
ID O9GZPO.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Spinal cord-derived growth factor-B (MSTP036) (Placental-derived growth
DE factor D) (Iris-expressed growth factor long form).
GN Name=hSCDGF-B; Synonyms=IEGF, PDGFD;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/brc.2000.4187;
RA Hamada T., Ue-Tel K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
RT SCDGF/PDGF-C/fallotenein.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liaw C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=2131380; PubMed=11331882; DOI=10.1038/35074593;
RA Larochelle W.J., Jeffers M., McDonald W.F., Chiklaku R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez B., Deegler L.L., Rittman B., Shinkens J.,
RA Shinkens R.A., Rothberg J.W., Lichenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor.";
RL Nat. Cell Biol. 3:517-521(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=1131181; DOI=10.1038/35074588;
RA Bergstein E., Uetela M., Li X., Plettras K., Ostman A., Heldin C.H.,
RA Alltalo K., Eriksson U.;
RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
RT receptor.";
RL Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RX MEDLINE=22103462; PubMed=12107412;
RA Wisnow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
RA Bouffard G., Smith D., Peterson K.;
RT "Expressed sequence tag analysis of adult human iris for the NEIBank
RT Project: steroid-response factors and similarities with retinal
RT pigment epithelium.";
RL Mol. Vision 8:185-195(2002).
DR EMBL: AB033833; BAB18903.1; -
DR EMBL: AF133216; AAG39287.1; -
DR EMBL: AF335584; AAK38840.1; -
DR EMBL: AF336376; AAK56136.1; -
DR EMBL: AY027517; AAK20081.1; -
DR PIR: JC7591; JC7591.
RN HSSD: O9JUS8; INT0.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0008083; F:growth factor activity; IEA.
DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000072; PD growth factor.
DR InterPro: IPR010916; TONB_Box_N.
DR Pfam: PF00431; CUB; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.

```

```

DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS0278; PDGF_2; 1.
DR PROSITE: PS0430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 370 AA; 42648 MW; D387F465E7B87674_CNC64;
Query Match 100.0%; Score 194; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 7,7e-142;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLEFYVTLICANFCSCRDTSATPOSASIKALRNANLRRESNHLQDLYRDETIQVKG 60
DB 1 MHRLEFYVTLICANFCSCRDTSATPOSASIKALRNANLRRESNHLQDLYRDETIQVKG 60
QY 61 NGVQSPRPFPNSYPNNLLTLWRHLSQENTRIQLVFDNQGLEAEMNDICRYDFVEVDIS 120
DB 61 NGVQSPRPFPNSYPNNLLTLWRHLSQENTRIQLVFDNQGLEAEMNDICRYDFVEVDIS 120
QY 121 ETSITIRGRWCGHKEVPRPKRSRTNQIKITKSDDYFVAKGFKIYSLLEDPOPAASE 180
DB 121 ETSITIRGRWCGHKEVPRPKRSRTNQIKITKSDDYFVAKGFKIYSLLEDPOPAASE 180
QY 181 TNWESVTSISGVSNPSVTDPPTLIADALDKIAEPTVEDLKYFNPESQOEDLEMY 240
DB 181 TNWESVTSISGVSNPSVTDPPTLIADALDKIAEPTVEDLKYFNPESQOEDLEMY 240
QY 241 LDTPRYRGRSYHDRKSKYVDLRLNDADAKRYSCTRPNYSVNIREBELKANVFFPRCLLVQ 300
DB 241 LDTPRYRGRSYHDRKSKYVDLRLNDADAKRYSCTRPNYSVNIREBELKANVFFPRCLLVQ 300
QY 301 RCGNGCGCGITVNMWSTCTNSGKYVKYHEVLQEPFGHKKRGRAKTALVLDLHDHRC 360
DB 301 RCGNGCGCGITVNMWSTCTNSGKYVKYHEVLQEPFGHKKRGRAKTALVLDLHDHRC 360
QY 361 DCICSSRPFR 370
DB 361 DCICSSRPFR 370
RESULT 2
O9BWVS PRELIMINARY: PRT: 364 AA.
ID O9BWVS.
AC O9BWVS.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Iris-expressed growth factor short form (Platelet derived growth
DE factor D, isoform 2) (SCDGF-B).
GN Name=IEGF; Synonyms=PDGFD; ORFNames=UNQ1899;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RX MEDLINE=22103462; PubMed=12107412;
RA Wisnow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
RA Bouffard G., Smith D., Peterson K.;
RT "Expressed sequence tag analysis of adult human iris for the NEIBank
RT Project: steroid-response factors and similarities with retinal
RT pigment epithelium.";
RL Mol. Vision 8:185-195(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usetin T.B., Toshimuki S., Carninci P., Prange C.,

```

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalak U., Smalins D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RA Strausberg R.;
RN Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RP [4]
RX SEQUENCE FROM N.A.
RA MEDLINE=22867296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gunney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seabright S., Simons L., Singh J., Smith V., Stinson J., Vagstad A.,
RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.H., Yatsuta D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL: AY027518; AAK20082.1; -;
DR EMBL: BC030645; AAH30645.1; -;
DR EMBL: AY359116; AAO89474.1; -;
DR PIR: JCT591; JCT591.
DR HSSP: Q9JUS8; LNT0.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0008083; F:growth factor activity; IEA.
DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000072; PD growth factor.
DR InterPro: IPR010916; TONB_Box_N.
DR Pfam: PF00431; CUB; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF 2; 1.
DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 364 AA; 42166 MW; 245C53B8DDEA9EAC_CRC64;

Query Match 97.7%; Score 1949; DB 2; Length 364;
Best Local Similarity 98.4%; Pred. No. 1.8e-138;
Matches 364; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MHRLLIVYLLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLVRRETIQVKG 60
DB 1 MHRLLIVYLLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLVRRETIQVKG 54
QY 61 NGVQSPRPFPNSYPRNLLTWRLHSGENTRIQLVFNQGLBEAENDICRYDVEVEDIS 120
DB 55 NGVQSPRPFPNSYPRNLLTWRLHSGENTRIQLVFNQGLBEAENDICRYDVEVEDIS 114
QY 121 ETSITIRGRWCGHKEVPRIKSRITNQIKITPKSDYFVAKPGFKIYYSLEDFQPAASE 180
DB 115 ETSITIRGRWCGHKEVPRIKSRITNQIKITPKSDYFVAKPGFKIYYSLEDFQPAASE 174
QY 181 TNMESVTSISGVSYSNPSVPTDPTLLADALDKKIAEDTVEDLLKYNPESWODELENNY 240
DB 175 TNMESVTSISGVSYSNPSVPTDPTLLADALDKKIAEDTVEDLLKYNPESWODELENNY 234
QY 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIIBELKLANVFFPRCLVQ 300

DB 235 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIIBELKLANVFFPRCLVQ 294
QY 301 RCGGNGCGCTVWNRSCCTGSKTKVKKYHEVLOEPFHRIKRGAKTMALVDIOLDHHERC 360
DB 295 RCGGNGCGCTVWNRSCCTGSKTKVKKYHEVLOEPFHRIKRGAKTMALVDIOLDHHERC 354
QY 361 DCICSSRPR 370
DB 355 DCICSSRPR 364

RESULT 3
Q9EQT1 PRELIMINARY; PRT; 370 AA.
ID 09EQT1;
AC 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal-cord derived growth factor-B.
GN Name=SCDGF-B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/dbrc.2000.4187;
RA Hamada T., Ue-Tel K., Imaki U., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
RT SCDGF/PDGF-C/fallicetin.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
DR EMBL: AB052170; BAB18920.1; -;
DR PIR: JCT592; JCT592.
DR HSSP: Q9UCV4; INZ1.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0008083; F:growth factor activity; IEA.
DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00431; CUB; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF 2; 1.
SQ SEQUENCE 370 AA; 42809 MW; 7BB8A251F679BF73_CRC64;

Query Match 89.0%; Score 1775; DB 2; Length 370;
Best Local Similarity 86.8%; Pred. No. 2.3e-125;
Matches 321; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 1 MHRLLIVYLLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLVRRETIQVKG 60
DB 1 MHRLLIVYLLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLVRRETIQVKG 60
QY 61 NGVQSPRPFPNSYPRNLLTWRLHSGENTRIQLVFNQGLBEAENDICRYDVEVEDIS 120
DB 61 TGVQSPRPFPNSYPRNLLTWRLHSGENTRIQLVFNQGLBEAENDICRYDVEVEDIS 120
QY 121 ETSITIRGRWCGHKEVPRIKSRITNQIKITPKSDYFVAKPGFKIYYSLEDFQPAASE 180
DB 121 ETSITIRGRWCGHKEVPRIKSRITNQIKITPKSDYFVAKPGFKIYYSLEDFQPAASE 180
QY 181 TNMESVTSISGVSYSNPSVPTDPTLLADALDKKIAEDTVEDLLKYNPESWODELENNY 240
DB 181 TNMESVTSISGVSYSNPSVPTDPTLLADALDKKIAEDTVEDLLKYNPESWODELENNY 240
QY 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIIBELKLANVFFPRCLVQ 300
DB 241 MOTPRYRGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIIBELKLANVFFPRCLVQ 300
QY 301 RCGGNGCGCTVWNRSCCTGSKTKVKKYHEVLOEPFHRIKRGAKTMALVDIOLDHHERC 360
DB 301 RCGGNGCGCTVWNRSCCTGSKTKVKKYHEVLOEPFHRIKRGAKTMALVDIOLDHHERC 360

OY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 4
ID 092517 PRELIMINARY; PRT: 370 AA.
OY 092517; Q9D1B; (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Platelet-derived growth factor D (Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003109
DE product:platelet-derived growth factor D).
GN Name:Pgfd.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
RA Lacrochelle W.J., Jeffers M., McDonald W.F., Chiklaku R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Bugess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkens J.,
RA Shinkens R.A., Rochberg J.M., Lichtenstein H.S.;
RT "PDGF D, A Novel Proteinase-Activated Growth Factor";
RL Nat. Cell Biol. 3:517-521(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning";
RL Meth. Enzymol. 303:19-44(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085560; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium,
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499774; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
RA Komori H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Komori H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kondo M., Koya S., Kunita R., Ohno M.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Soegabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335583; AAK38839.1; -
DR EMBL; AK003359; BAB22735.2; -
DR HSSP; Q9JUS8; 1NTO.
DR MGP; MG1:1919035; Pgfd.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SMO0141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF; 2; 1.
SQ SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBF CRC64;

Query Match 87.1%; Score 1737; DB 2; Length 370;
Best Local Similarity 85.1%; Pred. No. 1.7e-122;
Matches 315; Conservative 25; Mismatches 30; Indels 0; Gaps 0;

OY 1 MHRLEFVYTLICANFCSCRDTSATPQASIALRNANLRRESNHLTDLRYRDETYQKG 60
Db 1 MQRVLVLSILLCANFSCYPTDFATPQASIALRNANLRRESNHLTDLRYREENIQVTS 60
OY 61 NGVOSPEFNSYPRNLLTLRLHSGEWTRIOLVNDNFGLEBENDICRDFVEVEIS 120
Db 61 NGHVOSPEFNSYPRNLLTLRLHSGEWTRIOLVNDNFGLEBENDICRDFVEVEIS 120
OY 121 ETSITIRGMCQHEVPRISRTNQIKITEKSDYFAKKGFKIYSLLEDFCPAAASE 180
Db 121 EESTYVRRCMGHKEIPRISRTNQIKITEKSDYFAKKGFKIYFVEDFQEEAASE 180
OY 181 TNMESVTSSISGVSYNSPVTPTLIADALDKIAEFTVEDLKYFNPESQEDLENNY 240
Db 181 TNMESVTSSISGVSYNSPVTPTLIADALDKIAEFTVEDLKYFNPESQEDLENNY 240
OY 241 LDTPRYGRSYHDRSKYVDLRLNDARVSCPTPNYSVNIRESLKLNVVFFPCLLVQ 300
Db 241 LDTPRYGRSYHDRSKYVDLRLNDARVSCPTPNYSVNIRESLKLNVVFFPCLLVQ 300
OY 301 RCGNGCGGTNNMRSCTGNSGTVKKAHEVQFEGHIIKRGRAKTMAVLDIOLDHFRRC 360
Db 301 RCGNGCGGTNNMRSCTGNSGTVKKAHEVQFEGHIIKRGRAKTMAVLDIOLDHFRRC 360
OY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 5
OY 06V9H4 PRELIMINARY; PRT: 300 AA.
ID 06V9H4
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE It's-expressed growth factor (fragment).
GN Name:Pgfd;

```
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A.
RA Ray S., Mielow G.
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY347260; AAQ24382.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 1
FT TER 300
SQ SEQUENCE 300 AA; 34616 MW; 716C873C9C01C0C6 CRC64;

Query Match 74.3%; Score 1493; DB 2; Length 300;
Best Local Similarity 91.3%; Pred. No. 3e-104;
Matches 274; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 57 QVNGNGYVGSPPRPNYSRNLTLTWRLHSGENTRIQVFNQGLAEANDICRYDVEV 116
DB 1 QVNGNGYVGSPPRPNYSRNLTLTWRLHSGENTRIQVFNQGLAEANDICRYDVEV 60
QY 117 EDISSTIIIRGWCCKHEVPRIRKSTNOIKITFKSDDFVAKPGFKIYSLLEDFQPA 176
DB 61 EDISSTIIRGWCCKHEVPRIRKSTNOIKITFKSDDFVAKPGFKIYSLLEDFQPA 120
QY 177 AASETWESYTSISGVSYNSPSVTDPTLTADALDKKIAEFDTVEDLLKTFNPESQOEDL 236
DB 121 AASETWESYTSISGVSYNSPSVTDPTLTADALDKKIAEFDTVEDLLKTFNPESQOEDL 180
QY 237 ENNYLPTPRYGRSYPHDKSKVDLRLDNDKAKRYSCPRYSVNLREELKTLAVVPPRC 296
DB 181 ENNYLPTPRYGRSYPHDKSKVDLRLDNDKAKRYSCPRYSVNLREELKTLAVVPPRC 240
QY 297 LTVQRCGNGCGCTVWNRSCCTCNSGKTVKKYHEVLQPEFGHKKRGRAKTALVDIQLDH 356
DB 241 LTVQRCGNGCGCTVWNRSCCTCNSGKTVKKYHEVLQPEFGHKKRGRAKTALVDIQLDH 300

RESULT 6
O8K2L3 PRELIMINARY; PRT; 261 AA.
ID O8K2L3:
AC O8K2L3:
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Pdgfd protein.
GN Name=Pdgfd;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor;
RL MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleorn M., Soares M.B., Bonaldo M.F., Casavant T.L., Schiezel T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Caninici P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
```

```
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor;
RL Straubeberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030896; AAH30896.1; -.
DR HSSP; Q9JUS8; INT0.
DR MGD; MGI:1919035; Pdgfd.
DR GO; GO:0005615; C:extracellular space; TMS.
DR GO; GO:0050730; P:regulation of peptidyl-L-tyrosine phosphoryla. . . ; IDA.
DR InterPro; IPR000859; CUB.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
SQ SEQUENCE 261 AA; 30228 MW; 2EEC3F6373A52D09 CRC64;

Query Match 57.2%; Score 1141; DB 2; Length 261;
Best Local Similarity 82.5%; Pred. No. 7.8e-78;
Matches 212; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

QY 1 MHRLLVYTLICANFSCBDSATPOSASIKALRNANLRDESNHLLTDLYRRRETIQVKG 60
DB 1 MHRLLVYTLICANFSCBDSATPOSASIKALRNANLRDESNHLLTDLYRRRETIQVKG 60
QY 1 MQRVLVSLILCANFSCBDSATPOSASIKALRNANLRDESNHLLTDLYRRRETIQVKG 60
DB 1 MQRVLVSLILCANFSCBDSATPOSASIKALRNANLRDESNHLLTDLYRRRETIQVKG 60
QY 61 NGYVGSPPRPNYSRNLTLTWRLHSGENTRIQVFNQGLAEANDICRYDVEVEDIS 120
DB 61 NGYVGSPPRPNYSRNLTLTWRLHSGENTRIQVFNQGLAEANDICRYDVEVEDIS 120
QY 121 ERTSTIIIRGWCCKHEVPRIRKSTNOIKITFKSDDFVAKPGFKIYSLLEDFQPAASE 180
DB 121 ERTSTIIIRGWCCKHEVPRIRKSTNOIKITFKSDDFVAKPGFKIYSLLEDFQPAASE 180
QY 121 ESSTVIRGWCCKHEVPRIRKSTNOIKITFKSDDFVAKPGFKIYSLLEDFQPAASE 180
DB 121 ESSTVIRGWCCKHEVPRIRKSTNOIKITFKSDDFVAKPGFKIYSLLEDFQPAASE 180
QY 181 TWNESYTSISGVSYNSPSVTDPTLTADALDKKIAEFDTVEDLLKTFNPESQOEDL 240
DB 181 TWNESYTSISGVSYNSPSVTDPTLTADALDKKIAEFDTVEDLLKTFNPESQOEDL 240
QY 181 TWNESYTSISGVSYNSPSVTDPTLTADALDKKIAEFDTVEDLLKTFNPESQOEDL 240
DB 181 TWNESYTSISGVSYNSPSVTDPTLTADALDKKIAEFDTVEDLLKTFNPESQOEDL 240

QY 241 LDTPRYGRSYPHDKSK 257
DB 241 LDTPRYGRSYPHDKSK 257

RESULT 7
O91946 PRELIMINARY; PRT; 345 AA.
ID O91946:
AC O91946:
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=SCDGF;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=white leghorn; TISSUE=spinal cord;
RL MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ue-Tel K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
RT member of the PDGF/VEGF family.";
```

```

RL EBS Letc. 475:97-102(2000).
CC -i- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AB033829; BAB03265.1; -.
DR HSSP; O9JUS8; INT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000774; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000772; PD_growth_factor.
DR Pfam; PF00341; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR Growth factor; Mitogen.
KW SEQUENCE 345 AA; 38940 MW; 97ACEA92BF5128C CRC64;
SQ
Query Match 37.8%; Score 753; DB 2; Length 345;
Best Local Similarity 46.6%; Pred. No. 1,8e-48;
Matches 153; Conservative 54; Mismatches 91; Indels 30; Gaps 9;
QY 42 ESNHLTLYRDETTQVKGNGYVQSPFPNSYPRNLLTLWRHS-QEENTRIQLVFDNQG 100
DB 37 EONGVOD-FQHEKITVTNSGSIHSPKPHYPRNTVLVRLVAADENWIDLTEDERGG 95
QY 101 LEEAENDICRYDFVEVEDISESTIRGHWCGHKEVPRPKRTNOIKTFPSDDYFVK 160
DB 96 LDDPEDDICKYDFVEVEBPSDGTVL--GRWCGSSSVPSQISKNGDIRLRFVSDSEFPSPQ 153
QY 161 PEFKITYSLHEDFOPAAASETMSVESISISGVSNPSPTDPT-LIADALDKLIAEPT 219
DB 154 PEFCHITVLVHHTEAP-----SPSSLPSPALPLDVLNNAVAGET 195
QY 220 VEDLLKTFPESVQEDLEMYITDTPYRGST-HDRKSK-VLLDRINDAKYSCTPRNY 277
DB 196 VELRLRYLEPDMOJLDELYRPTWOLGKAYIHGKRKRVVDLNLKEEVRLLYSCPRNF 255
QY 278 SVNIREELKLVAVFPFRCLTVORCGNGCGTVMNRSTCNCSKTVKHYHVLQEPBH 337
DB 256 SVSLBELKRTDTTTPRLCLLVKRCGNGNACHONCNBCQCPRTVKYKHYHVLQKRP-- 313
QY 338 IKRRG-RAKTVALVDIQLDHERCDIC 364
DB 314 --RSGVRGLHKSLTVPLEHHECCVC 339
RESULT 8
Q90Y71 PRELIMINARY; PRT; 345 AA.
AC Q90Y71:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 28, Last annotation update)
DE Fallotien (Platelet-derived growth factor C) (Mus musculus adult male
DE cecum cDNA, RIKEN full-length enriched library, clone:913040008
DE product:platelet-derived growth factor, C polypeptide, full insert
DE sequence) (Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-
DE length enriched library, clone:A730022G11 product:platelet-derived
DE growth factor, C polypeptide, full insert sequence) (Mus musculus 15
DE days embryo head cDNA, RIKEN full-length enriched library,
DE clone:D930001M08 product:platelet-derived growth factor, C
DE polypeptide, full insert sequence).
DE Name=Pdgfr;
CN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
ID 11
RN SEQUENCE FROM N.A.
RP TISSUE=ovary;
RC

```

```

RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J;
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,
RA Gilbertson D., West J., O'Hara P.J.;
RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RL "Functional annotation of a full-length mouse cDNA collection.";
RN [5]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [6]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/Gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komori H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/Gr.152600;
RA Shibata K., Itoh M., Atzawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Komori H., Akiyama J., Nishi K., Katsuna T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Ozawa Y., Izawa M., Ohara E., Wachihi K.,
RA Yoneda Y., Ishikawa T., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RA Adachi J., Atzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Haneagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imochi K., Ishii Y., Itoh M., Kagawa I., Katsukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Komori H., Koda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishii K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -i- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF117608; AAF22516.1; -.
DR EMBL; AF266467; AAK58566.1; -.
DR EMBL; AK033734; BAC28455.1; -.
DR EMBL; AK042767; BAC31338.1; -.

```


DE Spinal cord-derived growth factor.
GN Name=rsdcgf;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar; TISSUE=Kidney;
RX MEDLINE=21092670; Pubmed=1162582; DOI=10.1006/bhrc.2000.4187;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDF-B, a novel growth factor homologous to
RT SCDF/PDGF-C/fallotectin";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AB031830; BAB1969.1; -.
DR HSP; Q9JUS8; INT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000559; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR Growth Factor; MitoGen.
SQ SEQUENCE 345 AA; 38734 MW; F296DAGE9B765D10 CRC64;

Query Match 37.3%; Score 744; DB 2; Length 345;
Best Local Similarity 45.3%; Pred. No. 8.6e-48;
Matches 148; Conservative 60; Mismatches 91; Indels 28; Gaps 10;

QY 42 ESNHLTDLRRDETIOVKGNGVQSPRPNSYRNLLTLWRHS-QENTRIQLVFDNQFG 100
DB 37 EQNGVQD-PRHBRVVTISGNGSIHSPKPHYPRNTVLWRLVAADENVRIGLTFDERG 95
QY 101 LEEAENDICRDYFVEVEDISSTIIIRGWCHEKVEPPRIKRTNQIKTFESDDYPAK 160
DB 96 LEDPDDDLCKXDFVEVEPSDSSV--GRWCSGTVPQKOTSKGHIIRIRFVSDYFPE 153
QY 161 PGCFIYSLLEDFOPAAASSETNWSVTSSISGVSNSPCVTDPTLLA-DALDKTAEPT 219
DB 154 PGCFIYSLI---MQVTETT-----SSVLPSPALSIDLNNAVTAFT 195
QY 220 VEDLLKYNFESQEDLENMYLDRPRYGRSY-HDRKSK-VLDRLNDAKRYSCTPRY 277
DB 196 VELLRIFLPDRWQIDLSLKYPTWPLLGKAPLYGKSKAVNLNLKEEVKLYSCTPRNF 255
QY 278 SVNIEELKLANVFFPRCLLVQRCGNGCGCTVWNRSTCNSGKTVKKYHVLQPEFGH 337
DB 256 SVSIEELKRDYTIFFWPGCLLVKRCGNCACCLHNCNEQCVPRVTKYKHEVLQLRP-K 314
QY 338 IKRRGRAKTMALVDIQLDHERCDCIC 364
DB 315 IGKGLHK--SLTDVALEHHECDVC 339

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=20461776; Pubmed=11004490; DOI=10.1016/S0167-4781(00)00066-X;
RA Tsai Y.J., Lee R.K., Lin S.P., Chon Y.H.;
RT "Identification of a novel platelet-derived growth factor-like gene,
RT fallotectin, in the human reproductive tract";
RL Biochim. Biophys. Acta 1492:196-202(2000).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20317014; Pubmed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
RN (3)
RP SEQUENCE FROM N.A.
RX MEDLINE=21347863; Pubmed=11297552; DOI=10.1074/jbc.M101056200;
RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
RA Holstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
RA Feldhaus A.L., Humes J.M., Palmer T.B., Hart C.E.;
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that
RL binds to PDGF alpha and beta receptor.";
RL J. Biol. Chem. 276:27406-27414(2001).
RN (4)
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; Pubmed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Devel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hoss P.E., Helens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis B., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yanesura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatic assessment.";
RL Genome Res. 13:2265-2270(2003).
RL EMBL; AF091434; AAF00049.1; -.
DR EMBL; AB033831; BAB03266.1; -.
DR EMBL; AF260738; AAK51637.1; -.
DR EMBL; AY358493; AAO88857.1; -.
DR HSP; Q9JUS8; INT0.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0008083; F:growth factor activity; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 37.2%; Score 742.5; DB 2; Length 345;
Best Local Similarity 43.6%; Pred. No. 1.1e-47;
Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

QY 5 IFVTLICANFCSDRDSATQASIKALRNANLRDRDSNHLTLDRDETIOVKGNGV 64
DB 3 LFGLLLSALAGQOGQOASNLSSKRFQSSN--KQNGVQD-PQHERITVTSTNGSI 58
QY 65 QSPFPNSYRNLLTLWRHS-QENTRIQLVFDNQFGEAENDICRDYFVEVEDISST 123
DB 59 HSPRPHPYPRNTVLWRLVAADENVRIGLTFDERFGLEDEDEDLCKXDFVEVEPSDGT 118
QY 124 TIIRGRCGHEKVEPPRIKRTNQIKTFESDDYPAKGFRIYSL-LEDQPAASSTN 182

Db 119 --ILGRWCGSGTVPKGQISKNGQIRIRFVSDXEPSEPGCHINYIMVQFTEAV----- 171
QY MESVTSISIGSVSNSSVYDPT-LIADALDKIAEFDYEDLLKYNPESWQEDLENMVL 241
Db 172 -----SSSVLPSPALPDLNLNNAITASTEDLLRYLEPERWQDLDBLYR 217
QY 242 DFRYGRSRY-HDRSKK-VLDRLNDADAKRSCTPNYSVINIEELKLANVFFPRCLY 259
Db 218 PTWQLLGKAFVPRKSRKRVLDNLITEEVRLYSCTPNFSVISEELKRTDTITWPGCLY 277
QY 300 QRCGNGCGGTVMNRSCCTCNSGKTVMKKEVLOFEPGHTKRRGRAKTMALVDIOLDHHR 359
Db 278 KRCGNGCACCLHNCNCCQVPSKYTKKYEVLQLRP---KTGVRGLHKSLTDVALBHEHE 334
QY 360 CDCIC 364
Db 335 CDCVC 339

RESULT 12

Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
GN Name=PDGfC;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
RA MEDLINE=20417814; PubMed=10960785; DOI=10.1016/S0925-4773(00)00425-1;
RX Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during
organogenesis";
RL Mech. Dev. 96:209-213(2000).
DR EMBL; AF286725; AAF91483.1; -.
DR HSSP; Q9JVS8; INTO.
DR MGD; MGI:1859631; PDGfC.
DR GO; GO:0005615; C:extracellular space; TAs.
DR GO; GO:0005461; F:platelet-derived growth factor receptor bin.; IDA.
DR GO; GO:0008284; P:regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla.; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin.; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 38866 MW; FA1486BD6D362T8 CRC64;

Query Match 37.2%; Score 742; DB 2; Length 345;
Best Local Similarity 45.0%; Pred. No. 1.2e-47;

Matches 147; Conservative 59; Mismatches 93; Indels 28; Gaps 9;

QY 42 ESNRLDLVDRDETIOVKNGVQSPRPNSYPRNLLTWRLHS-QENRIQLVFNQNG 100
Db 37 EQNGVOD-PREHVVITSGNGSIHSPKPHYPRNVLVAVDNVTQLTDFDRFG 95
QY 101 LEEAENDICRYDEVEEDISSTIIRGRWCGHKEVPRIKSRINOIKITFKSDDYFVAK 160
Db 96 LEEPDEDICKYDVEVEEPPDSGLV--GRWCGSETVPGKOTSKGNHRIKRVFVDEYFPE 153
QY 161 PGRKIYSLLEDPQPAALSTNWSVTSISGVSNSSVYDPT-LIADALDKIAEFDT 219
Db 154 PGCINHSII--MPQVTEY-----SSSVLPSPALPDLNLNNAITASTEDLLRYLEPERWQDLDBLYR 195

QY 220 VEDLTKEFNPEWQEDLENMVLDTPRYGRSY-HDRSKK-VLDRLNDADAKRSCTPRNY 277
Db 196 LEEILYLPEDPKQVLDLBYKPTWQLLGKAFYVYKSKVYNLILKEVEKLYSCTPRNF 255
QY 278 SVNIREELKLANVFFPRCLLYVRCGNGCGGTVMNRSCCTCNSGKTVMKKEVLOFEPGH 337
Db 256 SVSIREELKRTDTRFMFGCLLYVRGCGNACCLHNCNCCQVPSKYTKKYEVLQLRP-- 313
QY 338 IKRRGRAKTMALVDIOLDHNERCDCIC 364
Db 314 -KTGVKGLHKSLTDVALBHEHECDCVC 339

RESULT 13

Q9NRA1 PRELIMINARY; PRT; 345 AA.
AC Q9NRA1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20268201; PubMed=10806482; DOI=10.1038/35010579;
RA Li X., Ponten A., Aase K., Karlsson L., Abramson A., Uutela M.,
RA Backstrom G., Helstrom M., Boström H., Li H., Soriano P.,
RT "PDGFR-C is a new protease-activated ligand for the PDGFR alpha-
receptor";
RL Nat. Cell Biol. 2:302-309(2000).
CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF244813; AAF80597.1; -.
DR HSSP; Q9JVS8; INTO.
DR Genew; HGNC:8801; PDGRC.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55C5EA CRC64;

Query Match 37.2%; Score 741.5; DB 2; Length 345;
Best Local Similarity 43.6%; Pred. No. 1.3e-47;

Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

QY 5 IFVYLLICANFGSCRDTSATPOSASIKALRANLRDESNHLTDLVRDETIOVKNGVY 64
Db 3 LFGLLLVTSALAGRGTOAESNLSSKQFSSN---KEQNGVOD-PQHEIITVSTGSI 58
QY 65 QSPRPNSYPRNLLTWRLHS-QENRIQLVFNQNGLEAENDICRYDVEVEEDISSETS 123
Db 59 HSPRPHTYPRNVLVAVDNVTQLTDFDRFGLEPDEDICKYDVEVEEPPDSGDT 118
QY 124 TIRGRWCGHKEVPRIKSRINOIKITFKSDDYFVAKPGRKIYSL-LDFQPAALSTN 182
Db 119 --ILGRWCGSGTVPKGQISKNGQIRIRFVSDXEPSEPGCHINYIMVQFTEAV----- 171
QY 183 MESVTSISIGSVSNSSVYDPT-LIADALDKIAEFDYEDLLKYNPESWQEDLENMVL 241
Db 172 -----SSSVLPSPALPDLNLNNAITASTEDLLRYLEPERWQDLDBLYR 217


```
FT DISULFID 514 526 By similarity.
FT DISULFID 522 535 By similarity.
FT DISULFID 537 550 By similarity.
FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 105 105 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 295 295 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 326 326 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 562 562 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 707 AA; 80673 MW; 1B6980D716DC9B8D CRC64;

Query Match
Best Local Similarity 42.5%; Score 189.5; DB 1; Length 707;
Matches 45; Conservative 18; Mismatches 38; Indels 5; Gaps 4;

QY 59 KNGGYQSPFPNSYPRNLLTWRLHSGENTRIQLVFDNQFGLAEANDICRYDFVEVD 118
DB 560 KUNGSTSPGWPEYPPNKKCIWQVAPYRISLKFQ-QF--ETEGNDVCKYDFVEVRS 616
QY 119 ISETSTIIRGRCGHEVPPRIKSRNQIKITFKSDDYVAKGPF 164
DB 617 GLTSDSKLHGKFCG-SELPAVITSOYNNMRIEFSKN-TVSKKGFG 660

RESULT 16
Q91925 PRELIMINARY; PRT; 977 AA.
AC Q91925;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE xtd protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
NCBI_TaxID=8355;
RX NCB1_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Lin J., Maeda R., Ong R., Kim J., Kung H., Maeno M.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D83476; BA011922.1; -.
DR HSSP; P01130; 1H28.
DR GO; GO:0008533; F-actin activity; IEA.
DR GO; GO:0005509; F-actin monomer binding; IEA.
DR GO; GO:0008237; F-actin monomer binding; IEA.
DR GO; GO:0005508; P-protein synthesis; IEA.
DR Pfam; PF01400; CUB; 5.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF07645; EGF_CA_1.
DR PRINTS; PRO0480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZMGC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS0026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 977 AA; 110199 MW; 4D7D2E37C64FDF1F CRC64;

Query Match
Best Local Similarity 42.5%; Score 189.5; DB 2; Length 977;
Matches 45; Conservative 18; Mismatches 38; Indels 5; Gaps 4;

QY 59 KNGGYQSPFPNSYPRNLLTWRLHSGENTRIQLVFDNQFGLAEANDICRYDFVEVD 118
DB 588 KUNGSTSPGWPEYPPNKKCIWQVAPYRISLKFQ-QF--ETEGNDVCKYDFVEVRS 644
QY 119 ISETSTIIRGRCGHEVPPRIKSRNQIKITFKSDDYVAKGPF 164
```

```
DB 645 GLTSDSKLHGKFCG-SELPAVITSOYNNMRIEFSKN-TVSKKGFG 668

RESULT 17
Q57381 PRELIMINARY; PRT; 735 AA.
AC Q57381;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bone morphogenetic protein 1b.
GN Name=BMP-1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
NCBI_TaxID=8355;
RX NCB1_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ovary;
RA Goodman S., Albano R., Matthews G., Tannahill D., Dale L.;
RT "BMP-1 related proteins promote the development of ventral mesoderm in
RT early Xenopus embryos."
RL Dev. Biol. 194;144-157(1998).
DR EMBL; Y09660; CAA70853.1; -.
DR HSSP; P01130; 1H28.
DR GO; GO:0008533; F-actin activity; IEA.
DR GO; GO:0005509; F-actin monomer binding; IEA.
DR GO; GO:0008237; F-actin monomer binding; IEA.
DR GO; GO:0005508; P-protein synthesis; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006026; Peptidease M.
DR InterPro; IPR001506; Peptidease M12A.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 3.
DR Pfam; PF07645; EGF_CA; 1.
DR PRINTS; PRO0480; ASTACIN.
DR SMART; SM00042; CUB; 3.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00235; ZMGC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS0026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 735 AA; 83575 MW; 45B29C813F79DBE2 CRC64;

Query Match
Best Local Similarity 42.5%; Score 188.5; DB 2; Length 735;
Matches 45; Conservative 18; Mismatches 38; Indels 5; Gaps 4;

QY 59 KNGGYQSPFPNSYPRNLLTWRLHSGENTRIQLVFDNQFGLAEANDICRYDFVEVD 118
DB 587 KUNGSTSPGWPEYPPNKKCIWQVAPYRISLKFQ-QF--ETEGNDVCKYDFVEVRS 643
QY 119 ISETSTIIRGRCGHEVPPRIKSRNQIKITFKSDDYVAKGPF 164
DB 644 GLTSDSKLHGKFCG-SELPAVITSOYNNMRIEFSKN-TVSKKGFG 687

RESULT 18
Q66K13 PRELIMINARY; PRT; 735 AA.
AC Q66K13;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
```

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE BMP-1 protein.
GN Name=BMP-1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stabileton M., Soares M.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosch S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey U., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gernard D.S.,
RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC080382; AAH80382.1; -
DR InterPro: IPR000152; Asx_hydroxyl_S.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR006026; Peptidase_M.
DR InterPro: IPR001506; Peptidase_M12A.
DR InterPro: IPR006025; Pept_M_zn_BS.
DR Pfam: PF01400; Astacin; 1.
DR Pfam: PF00431; CUB; 3.
DR Pfam: PF00008; EGF; 1.
DR Pfam: PF07645; EGF_CA; 1.
DR PRINTS: PRO0480; ASTACIN.
DR SMART: SM00042; CUB; 3.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00235; ZmC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS01180; CUB; 3.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 735 AA; 83603 MW; 3D24DF66A4FABE64 CRC64;

Query Match 9.5%; Score 188.5; DB 2; Length 735;

Best Local Similarity 42.5%; Pred. No. 1.5e-05;
Matches 45; Conservative 18; Mismatches 38; Indels 5; Gaps 4;
QY 59 KGNVYOSPPRPNSYPNRLLLTWRLHSGOENRIQLVFNQGLAEANDIRYPVEVD 118
DB 587 KLNSTSPGWPKEKPPKNCVWLVAFTQYRISLKP-QF--ETEGNDVCKYDFEVR 643
QY 119 ISETSTIRGRGCGHKEVPPIKSRNTQIKITFKSDVPFAKPGPK 164
DB 644 GLTSDSKLHGKFCG-TFLPAVITSGYNNMRLEFKSDN-TVSKKGRQ 687
RESULT 19
ID 08J128 PRELIMINARY; PRT; 1007 AA.
AC 08J128;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Xoloid-like metalloprotease.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22352451; PubMed=12464431; DOI=10.1016/S0925-4773(02)00359-3;
RA Dale L., Evans W., Goodman S.A.,
RT "Xoloid-related: A novel BMP1/Toloid-related metalloprotease
RT expressed during early Xenopus development."
RL Mech. Dev. 119:177-190 (2002).
DR EMBL: AF393242; AAM73675.1; -
DR HSRP: P00736; IABQ.
DR MEROPS: M2.016; -
DR GO: GO:0008533; F:calcium activity; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0008237; F:metalloprotease activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR00152; Asx_hydroxyl_S.
DR InterPro: IPR00859; CUB.
DR InterPro: IPR00742; EGF_2.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR006026; Peptidase_M.
DR InterPro: IPR001506; Peptidase_M12A.
DR InterPro: IPR006025; Pept_M_zn_BS.
DR Pfam: PF01400; Astacin; 1.
DR Pfam: PF00431; CUB; 5.
DR Pfam: PF00008; EGF; 1.
DR Pfam: PF07645; EGF_CA; 1.
DR PRINTS: PRO0480; ASTACIN.
DR SMART: SM00042; CUB; 5.
DR SMART: SM00179; EGF_CA; 2.
DR SMART: SM00235; ZmC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 2.
DR PROSITE: PS01180; CUB; 5.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS00026; EGF_3; 2.
DR PROSITE: PS01187; EGF_CA; 2.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW EGF-like domain; Metalloprotease; Protease.
SQ SEQUENCE 1007 AA; 114364 MW; 3F3C666A7EF230C CRC64;
Query Match 9.5%; Score 188.5; DB 2; Length 1007;
Best Local Similarity 22.3%; Pred. No. 2.2e-05;
Matches 81; Conservative 44; Mismatches 118; Indels 121; Gaps 16;
QY 13 ANFCSCRTSATPQAS-----IKALRNANLRDESNHLLTDLVRRDET----IQVKNQY 63
DB 564 ANFLKEDECCARPDPGCGEGRQVNTLGSYKSCDGYELAPDKSCFAACGALLTKLNGT 623
QY 64 VQSPRPNSYPNRLLLTWRLHSGOENRIQLVFNQGLAEANDICRYDFVEVDISSETS 123

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:31:47 : Search time 165 Seconds
(without alignments)
867.281 Million cell updates/sec

Title: US-10-606-055-2

Perfect score: 370

Sequence: 1 MHRILFVYLICANFCSCRD.....DIQLDHERCDICSSRPPR 370

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size: 5

Total number of hits satisfying chosen parameters: 74988

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database:

A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	100.0	370	3	AA996864
2	370	100.0	370	3	AA848653
3	370	100.0	370	3	AA771130
4	370	100.0	370	4	AA660888
5	370	100.0	370	4	AAU00704
6	370	100.0	370	4	AAU00698
7	370	100.0	370	4	AA655601
8	370	100.0	370	4	AAE00999
9	370	100.0	370	4	AA855529
10	370	100.0	370	5	AAE15819
11	370	100.0	370	5	AB796643
12	370	100.0	370	5	ABG92893
13	370	100.0	370	5	ABA47891
14	370	100.0	370	5	AB879588
15	370	100.0	370	5	ABG78502
16	370	100.0	370	5	ABG76575
17	370	100.0	370	5	ABG64733
18	370	100.0	370	5	ABP51640
19	370	100.0	370	6	ABU72430
20	370	100.0	370	6	ABG76397
21	370	100.0	370	6	ABR80134
22	370	100.0	370	6	ABR43944
23	370	100.0	370	7	AAE38476
24	370	100.0	370	7	ABW02697
25	370	100.0	370	7	ADG47746

26	370	100.0	370	8	ADJ32755
27	370	100.0	370	8	ADL78000
28	370	100.0	370	8	ADL67182
29	370	100.0	370	8	ADL18360
30	370	100.0	370	8	ADM57643
31	370	100.0	370	8	ADO20113
32	370	100.0	370	8	ADR31427
33	368	99.5	368	7	ADG65193
34	347	93.8	347	7	ADK68120
35	347	93.8	347	7	ADR49109
36	323	87.3	323	4	AAU12264
37	323	87.3	323	4	AAE15820
38	323	87.3	323	5	AB884973
39	323	87.3	323	5	AB895579
40	323	87.3	323	5	ABO17708
41	323	87.3	323	6	ABU80962
42	323	87.3	323	6	ABU66662
43	323	87.3	323	6	ABU59743
44	323	87.3	323	6	ABO24933
45	323	87.3	323	6	ABU66938
46	323	87.3	323	6	ADA45705
47	323	87.3	323	6	ADA76136
48	323	87.3	323	6	ADA18786
49	323	87.3	323	6	ADA61409
50	323	87.3	323	6	ADBI9194
51	323	87.3	323	6	ADBI7735
52	323	87.3	323	6	ADBI8635
53	323	87.3	323	6	ADBI5778
54	323	87.3	323	6	ADA47564
55	323	87.3	323	6	ADA67359
56	323	87.3	323	6	ADBI3036
57	323	87.3	323	6	ADA85662
58	323	87.3	323	6	ADA68874
59	323	87.3	323	6	ADA91917
60	323	87.3	323	6	ADA87317
61	323	87.3	323	6	ADBI6519
62	323	87.3	323	6	ADA91611
63	323	87.3	323	6	ADBI4674
64	323	87.3	323	6	ADBI8635
65	323	87.3	323	6	ADA93850
66	323	87.3	323	6	ADBI9746
67	323	87.3	323	6	ADBI3058
68	323	87.3	323	6	ABO43241
69	323	87.3	323	6	ADA74312
70	323	87.3	323	6	ADBI24545
71	323	87.3	323	6	ADA82069
72	323	87.3	323	6	ADA75032
73	323	87.3	323	6	ADA85110
74	323	87.3	323	6	ADA84558
75	323	87.3	323	6	ADA829814
76	323	87.3	323	6	ADA80342
77	323	87.3	323	6	ADA75584
78	323	87.3	323	6	ADA46809
79	323	87.3	323	6	ADBI25105
80	323	87.3	323	6	ADBI3281
81	323	87.3	323	6	ADBI2631
82	323	87.3	323	6	ADBI0918
83	323	87.3	323	6	ADA60846
84	323	87.3	323	6	ADBI3993
85	323	87.3	323	6	ADA86322
86	323	87.3	323	6	ADA80894
87	323	87.3	323	6	ADA95770
88	323	87.3	323	6	ADBI6079
89	323	87.3	323	6	ADBI1564
90	323	87.3	323	6	ADA77343
91	323	87.3	323	6	ADBI8083
92	323	87.3	323	6	ADA86766
93	323	87.3	323	6	ADA87869
94	323	87.3	323	6	ADA46257
95	323	87.3	323	6	ADBI28287
96	323	87.3	323	6	ADBI28839
97	323	87.3	323	6	ADA76791
98	323	87.3	323	6	ADA88421

99 323 87.3 364 7 ADA97426
100 323 87.3 364 7 ADB27183

Ada97426 Human PRO
ADB27183 Human PRO

ALIGNMENTS

RESULT 1

AA96864
ID AA96864 standard; protein; 370 AA.

XX AA96864;

XX 26-SEP-2000 (first entry)

XX SEQ. ID. 37 from WO0034474.

XX Vascular endothelial growth factor; homologue; zvegf3; CUB domain;

XX Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;

XX chromosome 4q28.3; cytosolic; anti-psoriatic; anti-inflammatory;

XX anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;

XX vulnerable.

XX Homo sapiens.

XX WO200034474-A2.

XX 15-JUN-2000.

XX 07-DEC-1999; 99WO-US028968.

XX 07-DEC-1998; 98US-00207120.

XX 06-JUL-1999; 99US-0142576P.

XX 21-OCT-1999; 99US-0161653P.

XX 12-NOV-1999; 99US-0165255P.

XX (ZYMO) ZYMOGENETICS INC.

XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;

XX Gilbertson DG, West JW;

XX WPI; 2000-423420/36.

XX N-PSDB; AAS1541.

XX Novel zvegf3 polypeptides and nucleotides encoding them useful for

XX stimulating growth of smooth muscle cells and fibroblasts comprising an

XX epitope bearing portion of a specific amino acid sequence.

XX Disclosure; Page 164-165; 173pp; English.

XX Polypeptides comprising an epitope-bearing portion human or murine ZVEGF3

XX (vascular endothelial growth factor homologue) are claimed. The growth

XX factors comprise a growth factor domain and a CUB domain (generic

XX sequence motifs are shown in AA96863 and AA96860). The growth factor

XX domain is characterized by an arrangement of cysteine residues and beta-

XX strands that is characteristic of the "cysteine knot" structure of the

XX platelet-derived growth factor (PDGF) family. The CUB domain shows

XX homology to CUB domains in neuropilin, human bone morphogenetic protein-

XX 1, porcine seminal plasma protein, bovine acidic seminal fluid protein

XX and Xenopus laevis follid-like protein. Structural analysis and homology

XX predict that ZVEGF3 polypeptides complex with a second polypeptide to

XX form multimeric proteins. The human zvegf3 gene has been mapped to

XX chromosome 4q28.3. ZVEGF3 is useful for stimulating the growth of

XX fibroblasts or smooth muscle cells, for activating cell surface PDGF-

XX alpha receptor and for inhibiting PDGF-alpha receptor mediated cellular

XX processes. ZVEGF3 is useful for regulating (post-development) organ

XX growth, regeneration and maintenance, as well as tissue maintenance and

XX repair processes. ZVEGF3 antagonists are useful for treating cancer,

XX rheumatoid arthritis, diabetic retinopathy, ischemic limb disease, and

XX peripheral vascular disease, myocardial ischemia, vascular intimal

XX hyperplasia, atherosclerosis, wound healing, chronic liver disease and

XX haemangioma formation. ZVEGF3 can also be used to modulate neurite growth

XX and development of the nervous system, and for treating neurodegenerative

CC diseases
XX Sequence 370 AA;

Query Match 100.0%; Score 370; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLFFVYTLICANCSGCRDTSATPQASISAKLRANLRPDESNNLTDLRRDETIOYKG 60

DB 1 MHRLFFVYTLICANCSGCRDTSATPQASISAKLRANLRPDESNNLTDLRRDETIOYKG 60

QY 61 NGYVQSPRPFPNSYPENLLLTWRHLSQENTRIQLVFDNQFGEAENDICRYDFVEVDIS 120

DB 61 NGYVQSPRPFPNSYPENLLLTWRHLSQENTRIQLVFDNQFGEAENDICRYDFVEVDIS 120

QY 121 ETSITIRGRWCGHKEVPRIRKRTNQIKITRSDYFVAKGFKIYSLLEDFOFAASE 180

DB 121 ETSITIRGRWCGHKEVPRIRKRTNQIKITRSDYFVAKGFKIYSLLEDFOFAASE 180

QY 181 TNMESVTSISGVSNPSVTDPDLIADALDKIAEPDVEIDLKYPNPSQEDLENNY 240

DB 181 TNMESVTSISGVSNPSVTDPDLIADALDKIAEPDVEIDLKYPNPSQEDLENNY 240

QY 241 LDTPRYRGRSYHDKRSKYDLRLNDADAKRYSCTPRNYSVNI REBLKANVVFPRCLLVQ 300

DB 241 LDTPRYRGRSYHDKRSKYDLRLNDADAKRYSCTPRNYSVNI REBLKANVVFPRCLLVQ 300

QY 301 RCGNCGCGCTVNMWSCTNSGKTVKHYEVQFERGHIKRGKRAKTMALVDIQLDHHRC 360

DB 301 RCGNCGCGCTVNMWSCTNSGKTVKHYEVQFERGHIKRGKRAKTMALVDIQLDHHRC 360

QY 361 DCICSSRPFR 370

DB 361 DCICSSRPFR 370

RESULT 2

AA84653
ID AA84653 standard; protein; 370 AA.

XX AA84653;

XX 09-MAR-2001 (first entry)

XX Human growth factor homologue zvegf4, SHQ ID NO:2.

XX Human; zvegf4; growth factor homologue, VEGF/PDGF family; CUB domain;

XX PDGF-like activity; mitogenic; osteogenic; neovasculatization;

XX tissue repair; proliferation; differentiation; liver damage;

XX neurodegenerative; Alzheimer's disease; multiple sclerosis;

XX periodontal disease; bone fracture; wound healing; vulnerability; ischaemia;

XX immunomodulation; hepatic; chromosome 11q22.3-23.1.

XX Homo sapiens.

XX WO200066736-A1.

XX 03-MAY-2000; 2000WO-US040047.

XX 03-MAY-1999; 99US-00304216.

XX 10-NOV-1999; 99US-0164463P.

XX 04-FEB-2000; 2000US-0180169P.

XX (ZYMO) ZYMOGENETICS INC.

XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;

XX WPI; 2000-687541/67.

XX N-PSDB; AAC81555.

PT Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease.

XX Claim 1; Page 110-111; 143pp; English.

XX The invention relates to the human growth factor homologue zvegfg4
XX (AA88653), and nucleic acids encoding it (AAC81555). Zvegfg4 is a member
XX of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
XX growth factor) family. Zvegfg4 has a growth factor domain (AA848654)
XX characterised by a PDGF cysteine knot structure, and a CUB domain
XX (AA848655) which has a beta barrel structure. Zvegfg4 has PDGF-like
XX activity, having mitogenic activity on fibroblasts, vascular smooth
XX muscle cells and pericytes, and has also been shown to stimulate bone
XX growth. The invention also relates to fusion proteins comprising human
XX zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3
XX fusions; expression constructs and host cells comprising human zvegfg4
XX nucleic acids; the recombinant expression of human zvegfg4; an antibody
XX which binds to human zvegfg4 or a fragment thereof; a method of activating
XX a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a method
XX of modulating the proliferation, differentiation, migration or metabolism
XX of bone cells, comprising exposing bone cells to zvegfg4-derived
XX polypeptides; and a method of detecting a genetic abnormality in the
XX zvegfg4 gene of a patient. Zvegfg4 proteins and derived fragments may be
XX used to stimulate tissue development or repair, or cellular
XX differentiation or proliferation. They are particularly used for the
XX treatment or repair of liver damage, and may also be used to modulate
XX neurite growth (e.g., in the treatment of Alzheimer's disease or multiple
XX sclerosis). Due to their osteogenic activity, they may be used in the
XX treatment of periodontal disease and fractures. They may also be used to
XX enhance expansion and mobilisation of haematopoietic stem cells and
XX endothelial precursor stem cells, which may be useful in the treatment of
XX ischaemia, in wound healing, and in the modulation of the immune system.

XX The present sequence represents human zvegfg4

XX Sequence 370 AA;

XX Query Match 100.0%; Score 370; DB 3; Length 370;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 MHRLLFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIOVKG 60
XX |||||
XX 1 MHRLLFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIOVKG 60
XX
XX 61 NGVQSPRPFPNSYPRLNLLTWRLHSGQENTRIQLVFNQSGLEBAENDICRYDFVEVEDIS 120
XX |||||
XX 61 NGVQSPRPFPNSYPRLNLLTWRLHSGQENTRIQLVFNQSGLEBAENDICRYDFVEVEDIS 120
XX
XX 121 ESTTIRGRCGCKEVPRIKSTNOIKITFKSDDYFVAKRGKITYVSLLEDPQPAASG 180
XX |||||
XX 121 ESTTIRGRCGCKEVPRIKSTNOIKITFKSDDYFVAKRGKITYVSLLEDPQPAASG 180
XX
XX 181 TWNESVTSISGYSVSPVTDPTLLADALDKKIAEFVVEDLTKTFNPESQOEDENNY 240
XX |||||
XX 181 TWNESVTSISGYSVSPVTDPTLLADALDKKIAEFVVEDLTKTFNPESQOEDENNY 240
XX
XX 241 LDTPRYRGSYHDKRQVDLRLNDADAKRYSCTPRNYSVIRELKLAVNVFFPRLCIYV 300
XX |||||
XX 241 LDTPRYRGSYHDKRQVDLRLNDADAKRYSCTPRNYSVIRELKLAVNVFFPRLCIYV 300
XX
XX 301 RCGNGCGCGTVMNRSCCTNSGKTVKYYHEVLOFEPGHIRKGRGAKTMALVDIQLDHHRC 360
XX |||||
XX 301 RCGNGCGCGTVMNRSCCTNSGKTVKYYHEVLOFEPGHIRKGRGAKTMALVDIQLDHHRC 360
XX
XX 361 DCICSSRPFR 370
XX |||||
XX 361 DCICSSRPFR 370

XX RESULT 3
XX AA71130
XX AAY71130 standard; protein; 370 AA.

XX AC AAY71130;
XX DT 08-SEP-2000 (first entry)
XX DE Human Platelet Derived Growth Factor (PDGF)-D protein.

XX Platelet Derived Growth Factor-D; PDGF-D; human; cytotraffic; vulnery;
XX VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
XX proliferative; activator; proliferation; differentiation; motility;
XX growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
XX atherosclerosis; wound; metastasis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Domain 52..170
XX FT /label= CUB domain
XX FT /note= "Participates in protein-protein or carbohydrate
XX interactions"

XX FT Cleavage-site 254..257
XX FT /label= Proteolytic site
XX FT /note= "Dibasic motif"

XX PN MO200027879-A1.

XX 18-MAY-2000.

XX PF 10-NOV-1999; 99WO-US026462.

XX PR 10-NOV-1998; 98US-0107852P.

XX PR 28-DEC-1998; 98US-0113997P.

XX PR 26-AUG-1999; 99US-0150604P.

XX PR 04-OCT-1999; 99US-0157108P.

XX PR 05-OCT-1999; 99US-0157156P.

XX PA (LUDWIG) LUDWIG INST CANCER RES.

XX PI (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX PI Eriksson U, Aase K, Ponten A, Lee X, Ureia M, Alitalo K;

XX PI Oestman A, Heldin C;

XX DR WPI: 2000-376495/32.

XX DR N-PSDB; AAD00738.

XX PT Novel polynucleotides encoding a novel growth factor of cells expressing

XX PT a platelet-derived growth factor, useful for diagnostic and therapeutic

XX PT applications, e.g. concerning cancer.

XX PS Claim 25; Fig 8; 11pp; English.

XX The present sequence is the complete human platelet derived growth factor
XX (PDGF)-D, formally known as Vascular Endothelial Growth Factor (VEGF)-G.
XX It is derived from human foetal lung lamdaag10 cDNA library. It belongs
XX to the VEGF/PDGF family. It functions as an activator of proliferation,
XX differentiation, growth and motility of cells, that express PDGF-D
XX receptor. This sequence is useful for inhibiting the growth of tumours,
XX that express PDGF-D. Expression of PDGF-D and its proteolytic cleavage
XX for generating an activated truncated form is useful for regulating
XX receptor binding specificity of PDGF-D. PDGF-D antagonist is useful for
XX inhibiting tissue remodelling during the invasion of tumour cells into
XX normal cells. PDGF-D may be used to treat wounds, atherosclerosis,
XX metastasis and migration of smooth muscle cells

XX Sequence 370 AA;

XX Query Match 100.0%; Score 370; DB 3; Length 370;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 MHRLLFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIOVKG 60
XX |||||
XX 1 MHRLLFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIOVKG 60

```

QY 61 NGYVQSPREFPNSSYPNNLLLTWRLLHSQENTRIQLVFDNFGLEAEANDICRYDFVEVEDIS 120
Db 61 NGYVQSPREFPNSSYPNNLLLTWRLLHSQENTRIQLVFDNFGLEAEANDICRYDFVEVEDIS 120
QY 121 ETSIIIRGRWCGHKVEVPPRIKSRITNQIKITPKSDDYFVAKGPGFKIYSLLEDFOFAAASE 180
Db 121 ETSIIIRGRWCGHKVEVPPRIKSRITNQIKITPKSDDYFVAKGPGFKIYSLLEDFOFAAASE 180
QY 181 TNWESVTSISGVSNSPSVTDPTLLADALDKKIAEPDVEDDLKYNFNPESWQEDLENNY 240
Db 181 TNWESVTSISGVSNSPSVTDPTLLADALDKKIAEPDVEDDLKYNFNPESWQEDLENNY 240
QY 241 LDTPRYRGRSYHDRKSKYDLDRINDAKRYSCTPRNYSVINIREELKLANVVFPPRCLLVQ 300
Db 241 LDTPRYRGRSYHDRKSKYDLDRINDAKRYSCTPRNYSVINIREELKLANVVFPPRCLLVQ 300
QY 301 RCGNCGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNCGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

```

RESULT 4

AAB60888
ID AAB60888 standard; protein; 370 AA.

AC AAB60888;

DT 02-APR-2001 (first entry)

DE Human VEGF-G protein.

KW Vascular endothelial growth factor; VEGF; cancer; cell; angiogenesis.

XX Homo sapiens.

OS WO200100878-A2.

PN 04-JAN-2001.

PF 29-JUN-2000; 2000WO-US018085.

PR 30-JUN-1999; 99US-00343671.

PA (MILL-) MILLENNIUM PHARM INC.

PI Gearing DP;

DR WPI; 2001-050129/06.

XX New vascular endothelial growth factor family member used for diagnosis
PT and treatment of deregulated cell growth e.g. cancer, disorders involving
PT aberrant angiogenesis e.g. psoriasis, and chronic inflammatory diseases.

PS Claim 2; Fig 1; 142pp; English.

XX The present invention relates to a vascular endothelial growth factor
CC (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid molecules
CC are used as modulating agents or as targets for developing modulating
CC agents to regulate a variety of cellular processes e.g. cell

CC proliferation, differentiation, migration and wound repair. VEGF-G
CC modulators, i.e. VEGF-G protein, peptide, peptidomimetic or nucleic acid
CC are used to treat a subject with aberrant VEGF-G protein or nucleic acid
CC expression or activity e.g. deregulated cell growth, such as cancer,
CC hyperproliferative bone disorders, disorders involving aberrant angiogenesis
CC e.g. psoriasis, and chronic inflammatory diseases e.g. rheumatoid
CC arthritis. VEGF-G gene expression is inhibited through the administration
CC of antisense molecules or ribozymes and by targeting the regulatory
CC region of VEGF-G to prevent transcription of the gene in target cells

XX SQ Sequence 370 AA;

Query Match 100.0%; Score 370; DB 4; Length 370;

Beet Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MHRLLFVTLICANFCSGRDTSATPOSASIALRANLRDESNNLTDLVRDEETIQVKG 60
Db 1 MHRLLFVTLICANFCSGRDTSATPOSASIALRANLRDESNNLTDLVRDEETIQVKG 60
QY 61 NGYVQSPREFPNSSYPNNLLLTWRLLHSQENTRIQLVFDNFGLEAEANDICRYDFVEVEDIS 120
Db 61 NGYVQSPREFPNSSYPNNLLLTWRLLHSQENTRIQLVFDNFGLEAEANDICRYDFVEVEDIS 120
QY 121 ETSIIIRGRWCGHKVEVPPRIKSRITNQIKITPKSDDYFVAKGPGFKIYSLLEDFOFAAASE 180
Db 121 ETSIIIRGRWCGHKVEVPPRIKSRITNQIKITPKSDDYFVAKGPGFKIYSLLEDFOFAAASE 180
QY 181 TNWESVTSISGVSNSPSVTDPTLLADALDKKIAEPDVEDDLKYNFNPESWQEDLENNY 240
Db 181 TNWESVTSISGVSNSPSVTDPTLLADALDKKIAEPDVEDDLKYNFNPESWQEDLENNY 240
QY 241 LDTPRYRGRSYHDRKSKYDLDRINDAKRYSCTPRNYSVINIREELKLANVVFPPRCLLVQ 300
Db 241 LDTPRYRGRSYHDRKSKYDLDRINDAKRYSCTPRNYSVINIREELKLANVVFPPRCLLVQ 300
QY 301 RCGNCGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNCGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

```

RESULT 5

AAU00704
ID AAU00704 standard; protein; 370 AA.

AC AAU00704;

DT 07-SEP-2001 (first entry)

DE Human PDGFD protein.

KW Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;
KW VEGF-E; platelet derived growth factor; PDGF; FCTR; hyperplasia; cancer;
KW neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;
KW fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;
KW dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;
KW inflammatory disorder; Graft versus host disease; coagulation;
KW haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;
KW multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
KW peripheral neuropathy; acute brain injury.

OS Homo sapiens.

PN WO200125437-A2.

PD 12-APR-2001.

PF 06-OCT-2000; 2000WO-US027671.

PR 07-OCT-1999; 99US-0158083P.

PR 13-OCT-1999; 99US-0159231P.

PR 04-JAN-2000; 2000US-0174485P.

PR 03-MAR-2000; 2000US-0186707P.

PR 10-MAR-2000; 2000US-0188250P.

PR 08-AUG-2000; 2000US-0223879P.

PR 12-SEP-2000; 2000US-0066278P.

PR 20-SEP-2000; 2000US-0234082P.

PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Lichenstein H, Hermann JL, Boldog FL, Minskoff S;
 PI Jeffers M;
 XX
 DR WPI; 2001-316172/33.
 DR N-PSDB; AAS04498.
 XX
 PT Novel growth factor polypeptides termed as FCTR polypeptides, useful for
 PT treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
 PT wound healing and neuronal disorders.
 XX
 PS Disclosure; Fig 13: 171pp; English.
 XX
 CC The sequence represents a protein related to bone morphogenetic protein-1
 CC (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived
 CC growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1,
 CC VEGF-E and PDGF are referred to as FCTR polypeptides and nucleic acids.
 CC FCTR proteins are useful for treating or preventing a disorder
 CC associated with aberrant expression, aberrant processing, or aberrant
 CC physiological interactions of the proteins in a mammal, where the
 CC disorder is characterised by insufficient or ineffective growth of a cell
 CC or a tissue, e.g. hyperplasia or neoplasia. The peptides and their
 CC associated nucleic acids are useful for both promoting and inhibiting
 CC growth of cells and tissues and in treatment of cancer, anaemia,
 CC leukopenia, baldness, for treating cardiovascular and fibrotic disorders,
 CC diabetic ulcers, obesity, infectious diseases, hyperproliferative and
 CC dysproliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC inflammatory disorders, graft versus host disease, coagulation disorders
 CC such as haemophilia, and neural disorders including Parkinson's disease,
 CC Alzheimer's disease, multiple sclerosis, Huntington's disease,
 CC amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
 CC and epilepsy
 CC
 SQ Sequence 370 AA;
 Query Match 100.0%; Score 370; DB 4; Length 370;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNNHLDLYRDETIQVKG 60
 DB 1 MHRLLFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNNHLDLYRDETIQVKG 60
 QY 61 NGVQSPRPNSYPRLLLTWRLHSENRIOVFNQGLBEAENDICRYDVEVEDIS 120
 DB 61 NGVQSPRPNSYPRLLLTWRLHSENRIOVFNQGLBEAENDICRYDVEVEDIS 120
 QY 121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDDFVAKPGFKIYSLLEDEQPAASE 180
 DB 121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDDFVAKPGFKIYSLLEDEQPAASE 180
 QY 181 TWMESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDEVLKTFNPESWQEDLENNY 240
 DB 181 TWMESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDEVLKTFNPESWQEDLENNY 240
 QY 241 LDTPRRGRSGSYHDKSKVDLDRLNDADKRYSCTPRNYSVNIIRBELKIANVFFPRCLLYG 300
 DB 241 LDTPRRGRSGSYHDKSKVDLDRLNDADKRYSCTPRNYSVNIIRBELKIANVFFPRCLLYG 300
 QY 301 RCGGNGCGCTVNRSGCTCNSGKTVKKYHEVLQEPGHIKRGRAKTMALVDIQLDHHRC 360
 DB 301 RCGGNGCGCTVNRSGCTCNSGKTVKKYHEVLQEPGHIKRGRAKTMALVDIQLDHHRC 360
 QY 361 DCICSSRRPR 370
 DB 361 DCICSSRRPR 370

RESULT 6
 AAU00698
 XX AAU00698 standard; protein; 370 AA.
 XX

AC AAU00698;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human FCTR1 protein present in clone 30664188.0.99.
 XX
 XX Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;
 KW VEGF-E; platelet derived growth factor; PDGF; FCTR; hyperplasia; cancer;
 KW neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;
 KW fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;
 KW dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;
 KW inflammatory disorder; Graft versus host disease; coagulation;
 KW haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;
 KW multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
 KW peripheral neuropathy; acute brain injury.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /note="Signal peptide"
 FT Protein 24..370
 FT /note="Mature FCTR1"
 FT Domain 53..167
 FT /note="CUB domain"
 FT Domain 272..306
 FT /note="PDGF domain"
 FT Modified-site 276
 FT /note="N-linked glycosylation site"
 FT Domain 302..365
 FT /note="Metallothionein domain"
 FT Domain 350..362
 FT /note="PDGF domain"
 FT
 PN WO200125437-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 06-OCT-2000; 2000WO-US027671.
 XX
 XX 07-OCT-1999; 99US-0158083P.
 PR 13-OCT-1999; 99US-0159231P.
 PR 04-JAN-2000; 2000US-0174485P.
 PR 03-MAR-2000; 2000US-0186707P.
 PR 10-MAR-2000; 2000US-0188250P.
 PR 08-AUG-2000; 2000US-0223679P.
 PR 12-SEP-2000; 2000US-00662783.
 PR 20-SEP-2000; 2000US-0234082P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Lichenstein H, Hermann JL, Boldog FL, Minskoff S;
 PI Jeffers M;
 XX
 DR WPI; 2001-316172/33.
 DR N-PSDB; AAS04498.
 XX
 PT Novel growth factor polypeptides termed as FCTR polypeptides, useful for
 PT treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
 PT wound healing and neuronal disorders.
 XX
 PS Claim 1; Fig 1: 171pp; English.
 XX
 CC The sequence represents a protein related to bone morphogenetic protein-1
 CC (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived
 CC growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1,
 CC VEGF-E and PDGF are referred to as FCTR polypeptides and nucleic acids.
 CC FCTR proteins are useful for treating or preventing a disorder
 CC associated with aberrant expression, aberrant processing, or aberrant
 CC physiological interactions of the proteins in a mammal, where the
 CC disorder is characterised by insufficient or ineffective growth of a cell
 CC or a tissue, e.g. hyperplasia or neoplasia. The peptides and their
 CC associated nucleic acids are useful for both promoting and inhibiting

CC growth of cells and tissues and in treatment of cancer, anaemia,
CC leukopenia, baldness, for treating cardiovascular and fibrotic disorders,
CC diabetic ulcers, obesity, infectious diseases, hyperproliferative and
CC dysproliferative disorders, neurodegenerative disorders, osteoarthritis,
CC inflammatory disorders, graft versus host disease, coagulation disorders
CC such as haemophilia, and neural disorders including Parkinson's disease,
CC Alzheimer's disease, multiple sclerosis, Huntington's disease,
CC amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
CC and epilepsy

XX Sequence 370 AA;

Query Match 100.0%; Score 370; DB 4; Length 370;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MHRLLFYVTLICANFCSCRDTSATPQASISIKALRNANLRDESNHLLTDLYRRDETIQYKG 60
DB 1 MHRLLFYVTLICANFCSCRDTSATPQASISIKALRNANLRDESNHLLTDLYRRDETIQYKG 60
QY 61 NGYVQSPFPNPSYPNNLLLTWRLSOENTRIQLVFDNFGLEAENDICRYDFEVEDIS 120
DB 61 NGYVQSPFPNPSYPNNLLLTWRLSOENTRIQLVFDNFGLEAENDICRYDFEVEDIS 120
QY 121 ETSIIIRGMCQHKVEPPRIKSRITNQIKITPKSDDYFVAKPGFKIYSSLBEDFQPAASE 180
DB 121 ETSIIIRGMCQHKVEPPRIKSRITNQIKITPKSDDYFVAKPGFKIYSSLBEDFQPAASE 180
QY 181 TNWESVTSISIGVSNPSVTDPTLIADALDKKIAEFTVEDLLKYFPNDESOEDLENNY 240
DB 181 TNWESVTSISIGVSNPSVTDPTLIADALDKKIAEFTVEDLLKYFPNDESOEDLENNY 240
QY 241 LDTPEYRGRSYHDKRSKYVDLRLNDADAKRYSCTPPNYSVNIREEIKLANVVFPPCLLVQ 300
DB 241 LDTPEYRGRSYHDKRSKYVDLRLNDADAKRYSCTPPNYSVNIREEIKLANVVFPPCLLVQ 300
QY 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEFGHKKRGRAKTMALVDIQLDHHERC 360
DB 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEFGHKKRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370
```

RESULT 7

AA65601 ID AA65601 standard; protein; 370 AA.

XX AAC65601;

DT 07-JAN-2002 (first entry)

XX Human zvegfg4 polypeptide.

XX zvegfg4; bone; ligament; cartilage; osteoblast; osteoclast; chondrocyte;
KW bone cancer; osteonecrosis; bone defect; osteogenesis; osteoporosis;
KW osteopathic; vulnery; human.

XX Homo sapiens.

OS Homo sapiens.

XX Key

XX Location/Qualifiers

XX 1..18 /notes="secretory peptide"

XX 19..370 /notes="mature protein"

XX 52..179 /notes="CUB domain"

XX 180..257 /notes="propeptide-like sequence"

XX 258..370 /notes="growth factor domain"

PN WO200157083-A1.
XX 09-AUG-2001.
XX 03-MAY-2000; 2000WO-US012095.
XX 04-FEB-2000; 2000US-0180169P.
XX 31-MAR-2000; 2000US-00540224.
XX (ZYMO) ZYMOGENETICS INC.
XX Gilbertson DG, Hart CE;
XX WPI; 2001-611088/70.
XX N-PSDB; AAH47772.
XX Use of zvegfg4 polypeptide for promoting bone, ligament or cartilage
XX growth in mammal at site of fracture, implant, and bone graft, and for
XX promoting growth or differentiation of osteoblasts, chondrocytes in
XX culture.
XX Example 2; Page 44-47; 57pp: English.

CC The invention relates to the use of zvegfg4 polypeptide for promoting
CC bone, ligament or cartilage growth in a mammal, and for promoting
CC proliferation or differentiation of osteoblasts, osteoclasts,
CC chondrocytes or bone marrow stem cells in culture. For promoting
CC cartilage growth, chondrocytes are cultured ex vivo in presence of the
CC zvegfg4 polypeptide and then placed into mammal where cartilage is to be
CC grown. Zvegfg4 polypeptide is useful for promoting growth of bone,
CC ligament or cartilage in a mammal at a site of bony defect such as
CC fracture, bone graft, implant or periodontal pocket, in humans and non-
CC human animals such as domestic animals including livestock and companion
CC animals. Zvegfg4 is used for promoting growth of bone, ligament, or
CC cartilage in conditions of bone defects following therapeutic treatments
CC of bone cancers or other conditions characterized by increased bone loss
CC or decreased bone formation, or elevation of peak bone mass in pro-
CC menopausal woman. It is also useful for healing bone following radiation
CC -induced osteonecrosis, repairing bone defects arising from surgery, and
CC promotion of bone healing in plastic surgery, increasing bone formation
CC during distraction osteogenesis, treating bone injuries including repair
CC of cartilage and ligament and treatment of osteoporosis. The present
CC sequence represents a human zvegfg4 polypeptide

XX Sequence 370 AA;

Query Match 100.0%; Score 370; DB 4; Length 370;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MHRLLFYVTLICANFCSCRDTSATPQASISIKALRNANLRDESNHLLTDLYRRDETIQYKG 60
DB 1 MHRLLFYVTLICANFCSCRDTSATPQASISIKALRNANLRDESNHLLTDLYRRDETIQYKG 60
QY 61 NGYVQSPFPNPSYPNNLLLTWRLSOENTRIQLVFDNFGLEAENDICRYDFEVEDIS 120
DB 61 NGYVQSPFPNPSYPNNLLLTWRLSOENTRIQLVFDNFGLEAENDICRYDFEVEDIS 120
QY 121 ETSIIIRGMCQHKVEPPRIKSRITNQIKITPKSDDYFVAKPGFKIYSSLBEDFQPAASE 180
DB 121 ETSIIIRGMCQHKVEPPRIKSRITNQIKITPKSDDYFVAKPGFKIYSSLBEDFQPAASE 180
QY 181 TNWESVTSISIGVSNPSVTDPTLIADALDKKIAEFTVEDLLKYFPNDESOEDLENNY 240
DB 181 TNWESVTSISIGVSNPSVTDPTLIADALDKKIAEFTVEDLLKYFPNDESOEDLENNY 240
QY 241 LDTPEYRGRSYHDKRSKYVDLRLNDADAKRYSCTPPNYSVNIREEIKLANVVFPPCLLVQ 300
DB 241 LDTPEYRGRSYHDKRSKYVDLRLNDADAKRYSCTPPNYSVNIREEIKLANVVFPPCLLVQ 300
QY 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEFGHKKRGRAKTMALVDIQLDHHERC 360
DB 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEFGHKKRGRAKTMALVDIQLDHHERC 360
```

QY 361 DCICSSRPPR 370
 Db 361 DCICSSRPPR 370

RESULT 8
 ID AAE00999 standard; protein; 370 AA.
 AC AAE00999;
 DT 04-JUL-2001 (first entry)
 DE Human Zvegff protein which forms heteromultimer with Zvegfg protein.

XX Human; Zvegfg3 antagonist; cell proliferation; stellate cell activation;
 KW extracellular matrix production; fibrosis; VEGF-R; PDGF-C;
 KW platelet-derived growth factor; PDGF; vascular endothelial growth factor;
 KW VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;
 KW chronic active hepatitis; fulminant viral hepatitis; amyloidosis;
 KW diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;
 KW asbestosis; renal arteriosclerosis; post necrotic cirrhosis;
 KW diabetic glomerulosclerosis; focal glomerulosclerosis; hypertostosis;
 KW pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;
 KW bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;
 KW fibroproliferative disorder; Zvegfg4 protein.

XX Homo sapiens.
 XX MO200128586-A1.
 XX 26-APR-2001.
 XX 23-OCT-2000; 2000WO-US029270.
 XX 21-OCT-1999; 99US-0161653P.
 PR 12-NOV-1999; 99US-0165255P.
 PR 01-AUG-2000; 2000US-0222223P.
 XX (ZYMO) ZYMOGENETICS INC.
 PA Gilbertson DG;
 PI WPI; 2001-300278/31.
 DR Use of zvegfg3 antagonist for reducing fibroproliferative disorder of
 PT kidney, liver and bone, reducing extracellular matrix production,
 PT treating fibrosis or reducing stellate cell activation in mammal.
 XX
 XX Disclosure; Page 62-63; 70pp; English.

XX The patent discloses materials and methods for reducing cell
 CC proliferation or extracellular matrix production, treating fibrosis and
 CC reducing stellate cell activation in a mammal. The method comprises
 CC administering a composition containing a Zvegfg3 antagonist in combination
 CC with a delivery vehicle. The Zvegfg3 is a protein that is structurally
 CC related to platelet-derived growth factor (PDGF) and the vascular
 CC endothelial growth factors (VEGF). The Zvegfg3 protein is also designated
 CC as "VEGF-R" and "PDGF-C". The Zvegfg3 antagonist is useful to block the
 CC mitogenic effects of zvegfg3 and thereby to inhibit or prevent and treat
 CC keloids, scleroderma, fibrotic disorders of liver such as chronic active
 CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and alpha-1
 CC antitrypsin deficiency, fibrotic disorders of the kidney such as
 CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
 CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders
 CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,
 CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,
 CC fibrotic disorders of pancreas, fibroproliferative disorders of the
 CC vasculature such as transplant vasculopathy and fibroproliferative
 CC disorders of the bone such as osteopetrosis and hypertostosis. The present
 CC sequence is human Zvegfg4 protein which forms a heteromultimer with Zvegfg3
 CC protein

XX SQ Sequence 370 AA;
 Query Match 100.0%; Score 370; DB 4; Length 370;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFSCSDTSATPOSASIKALRNANLNRDESNHLLTDLYRRDETTQVNG 60
 Db 1 MHRLLFVYTLICANFSCSDTSATPOSASIKALRNANLNRDESNHLLTDLYRRDETTQVNG 60

QY 61 NGVQSPRPFPNSYPRNLLTLTWRLHSEENTRIQLVFNQFGLFEAENDICRYDVEVEDIS 120
 Db 61 NGVQSPRPFPNSYPRNLLTLTWRLHSEENTRIQLVFNQFGLFEAENDICRYDVEVEDIS 120

QY 121 ETSITIRGFWCGHKEVPRIKSRFTNQIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
 Db 121 ETSITIRGFWCGHKEVPRIKSRFTNQIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180

QY 181 TWMESTSSISGVSYNSPVTPTLADALDKIAEFDVDELKYPNESPQWEDLENMY 240
 Db 181 TWMESTSSISGVSYNSPVTPTLADALDKIAEFDVDELKYPNESPQWEDLENMY 240

QY 241 LPTPRYRGHSYHDRKSKVDLDRINDAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300
 Db 241 LPTPRYRGHSYHDRKSKVDLDRINDAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300

QY 301 RCGGNCGGCTVWNRSCCTNCGKTVKKYHEVLOFEPGHIYRGRGAKTMAVLDIOLDHHERC 360
 Db 301 RCGGNCGGCTVWNRSCCTNCGKTVKKYHEVLOFEPGHIYRGRGAKTMAVLDIOLDHHERC 360

QY 361 DCICSSRPPR 370
 Db 361 DCICSSRPPR 370

RESULT 9
 ID AAB85529 standard; protein; 370 AA.
 AC AAB85529;
 DT 25-SEP-2001 (first entry)
 DE Human secreted protein (clone Id HGCNC48).

XX Secreted protein; immunosuppressive; antiarthritic; antirheumatic;
 KW antiproliferative; cyostatic; cardiant; vasodilator; cerebroprotective;
 KW nootropic; neuroprotective; antibacterial; virucide; fungicide; human;
 KW ophthalmological; gene therapy.

XX Homo sapiens.
 XX MO200155430-A1.
 XX 02-AUG-2001.
 XX 17-JAN-2001; 2001WO-US001431.
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 12-SEP-2000; 2000US-0231968P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Komatsu GA, Baker KP, Birse CE, Soppet DR;
 PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;
 PI Fiscella M, Ni J, Ruben SM, Barash SC;
 DR WPI; 2001-476220/51.
 DR N-PSDB; AAH46939.
 XX 17 isolated nucleic acid molecules encoding human secreted proteins, used

PT to preventing, treating or ameliorating a medical condition.
XX
XX Claim 11; Page 447-449; 482pp; English.

XX The invention provides novel human secreted proteins and polynucleotides
CC encoding them. The secreted proteins can be expressed by standard
CC recombinant methodology. The secreted proteins and polynucleotides are
CC used to prevent, treat or ameliorate a medical condition in e.g. humans,
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can
CC also be used in diagnosing a pathological condition. The antibodies to
CC the proteins can also be used in alleviating symptoms associated with the
CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme
CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities. The present
CC sequence represents a human secreted protein

XX Sequence 370 AA;

Query Match 100.0%; Score 370; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLIFVYTLICANFCSCRODTSATPQASISALRNANRRDSENLTLVYRDETIOYKG 60
DB 1 MHRLLIFVYTLICANFCSCRODTSATPQASISALRNANRRDSENLTLVYRDETIOYKG 60
QY 61 NGYVQSPFPNPSYRNLLLTWRLHSEENTRIQVFDNFGLEAENDICRYDFVEVEDIS 120
DB 61 NGYVQSPFPNPSYRNLLLTWRLHSEENTRIQVFDNFGLEAENDICRYDFVEVEDIS 120
QY 121 ETSITIRGRWCGHKEVPPRIKSRITNQIKITFKSDDYFVAKPGFKIYSLLEDFOPAASE 180
DB 121 ETSITIRGRWCGHKEVPPRIKSRITNQIKITFKSDDYFVAKPGFKIYSLLEDFOPAASE 180
QY 181 TNWESVTSISGVSNPSVPTDPTLIADALDKKIAEPTVBDLKYFNPESQOELENNY 240
DB 181 TNWESVTSISGVSNPSVPTDPTLIADALDKKIAEPTVBDLKYFNPESQOELENNY 240
QY 241 LDTPRYGRSRVYHDKRSKYDLRLNDAKRYSCTPRNYSVNIIEELKANVVFPPRCLLVQ 300
DB 241 LDTPRYGRSRVYHDKRSKYDLRLNDAKRYSCTPRNYSVNIIEELKANVVFPPRCLLVQ 300
QY 301 RCGNGCGCGTVNWSCTCNSGKTVKKYHEVLOFEPFGHITKRRGAKTMALVLDIOLDHHERC 360
DB 301 RCGNGCGCGTVNWSCTCNSGKTVKKYHEVLOFEPFGHITKRRGAKTMALVLDIOLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 10

AAE15819
ID AAE15819 standard; protein; 370 AA.

XX AAE15819;

XX 26-MAR-2002 (first entry)

XX Human LP85 protein #1.

XX LP85; platelet-derived growth factor; PDGF; antiinflammatory; vulnerary;
KW osteopathic; neuroprotective; tranquilliser; musculoskeletal disorder;

KW MSD; therapy; bone growth; cartilage differentiation; wound healing;
KW neuron growth; bone fracture; osteoporosis; osteopenia; arthritis;
KW sarcopenia; periodontal disease; tissue atrophy; endocrine disorder;
KW muscle loss; immobility; bone density.

OS Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..12
FT /label= Signal_peptide
FT Protein 13..370
FT /label= Human_mature_LP85_protein

XX WO200189450-A2.

XX 29-NOV-2001.

XX 08-MAY-2001; 2001WO-US011755.

XX 19-MAY-2000; 2000US-0205424P.

XX 11-JAN-2001; 2001US-0261071P.

XX 11-JAN-2001; 2001US-0261076P.

XX (BUL) LILLY & CO ELI.

XX Beals JM, Gonzalez-Dewhitt PA, Hammond LJ, Lu J, Na S, Su EW;
PI Witcher DR, Wroblewski VJ;

XX WPI; 2002-083040/11.

XX N-PSDB; AAD15819.

PT Analog of a platelet-derived growth factor homolog, LP85 useful for
PT treating osteoporosis, arthritis, sarcopenia, wounds, has one or more
PT amino acid substitutions which destroy the tripeptidyl sequence of native
PT LP85.

PS Claim 11; Page 109-110; 117pp; English.

CC The present invention relates to LP85, an analogue of platelet-derived
CC growth factor (PDGF) homologue. Sequences of the invention are useful for
CC the manufacture of a medicament for treating musculoskeletal disorder
CC (MSD) which include promoting bone growth, cartilage differentiation and
CC function, wound healing, neuron growth, preventing cartilage degradation
CC or neuronal degeneration. They are useful for treating bone fractures,
CC osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease,
CC tissue atrophy, traumatised connective tissues, grafted connective
CC tissues and/or transplanted organs, bone or muscle loss due to
CC malignancy, endocrine disorders and immobility. They are also used for
CC prophylactically increasing or maintaining bone density in a mammal. The
CC present sequence is human LP85 protein

SQ Sequence 370 AA;

Query Match 100.0%; Score 370; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLIFVYTLICANFCSCRODTSATPQASISALRNANRRDSENLTLVYRDETIOYKG 60
DB 1 MHRLLIFVYTLICANFCSCRODTSATPQASISALRNANRRDSENLTLVYRDETIOYKG 60
QY 61 NGYVQSPFPNPSYRNLLLTWRLHSEENTRIQVFDNFGLEAENDICRYDFVEVEDIS 120
DB 61 NGYVQSPFPNPSYRNLLLTWRLHSEENTRIQVFDNFGLEAENDICRYDFVEVEDIS 120
QY 121 ETSITIRGRWCGHKEVPPRIKSRITNQIKITFKSDDYFVAKPGFKIYSLLEDFOPAASE 180
DB 121 ETSITIRGRWCGHKEVPPRIKSRITNQIKITFKSDDYFVAKPGFKIYSLLEDFOPAASE 180
QY 181 TNWESVTSISGVSNPSVPTDPTLIADALDKKIAEPTVBDLKYFNPESQOELENNY 240
DB 181 TNWESVTSISGVSNPSVPTDPTLIADALDKKIAEPTVBDLKYFNPESQOELENNY 240

QY	2.1	LDTPYRGRSSHYDRKSKVLDLRINDAKRYSCTPRNYSVINIRELKLAVNFFPRCLVQ	300
Db	2.1	LDTPYRGRSSHYDRKSKVLDLRINDAKRYSCTPRNYSVINIRELKLAVNFFPRCLVQ	300
QY	3.01	RCGSGCGGTVMWRSGCTCSNGKTVKKYKHEVLOPEPGHIKRGRAKTMALVDIOLDHHERC	360
Db	3.01	RCGSGCGGTVMWRSGCTCSNGKTVKKYKHEVLOPEPGHIKRGRAKTMALVDIOLDHHERC	360
QY	3.61	DCICSSRRPPR 370	
Db	3.61	DCICSSRRPPR 370	
RESULT 11			
ABB79643	1D	ABB79643 standard; protein; 370 AA.	
XX	AC	ABB79643;	
XX	DT	21-OCT-2002 (first entry)	
XX	DE	Human FCTRI (platelet derived growth factor D).	
XX	KW	FCTRI; platelet derived growth factor D; PDGFD; human; Crohn's disease;	
KW	KM	inflammatory bowel disease; gene therapy; antiinflammatory; vulnery;	
XX	XX	cystostatic; cardiovascular.	
XX	OS	Homo sapiens.	
XX	XX		
FH	Key	Location/Qualifiers	
FT	Peptide	1..23	
FT		/label= Signal_peptide	
FT	Protein	24..370	
FT		/label= Mature_protein	
FT	Domain	53..167	
FT		/note= "CUB domain"	
FT	Domain	272..306	
FT		/note= "PDGF domain"	
FT	Domain	302..365	
FT		/note= "metallothionein domain"	
FT	Domain	350..362	
FT		/note= "PDGF domain"	
XX	XX		
XX	PN	WO200258716-A2.	
XX	XX		
PD	01-AUG-2002.		
XX	XX		
PF	06-NOV-2001; 2001WO-US043846.		
XX	XX		
PR	06-NOV-2000; 2000US-0246206P.		
XX	XX		
PA	(CURA-) CURAGEN CORP.		
XX	XX		
P1	Jeffers M, Shimkets RA, Prayaga S, Boldog FL, Yang M, Burgess CF,		
P1	Fernandes ER, Rittman B, Shimkets JB, Larochelel WJ, Lichenstein HS;		
DR	WPI; 2002-599742/64.		
DR	N-PSDB; ABB84524.		
XX	XX		
PT	Treating, delaying the onset of, or ameliorating an inflammatory		
PT	pathology (e.g. inflammatory bowel disease or Crohn's disease) by		
PT	administering to the subject fibroblast growth factors or a combination		
PT	of growth factors.		
XX	XX		
PS	Claim 5; Page 19-21; 196pp; English.		
XX	XX		
CC	The present sequence is the protein sequence of human growth factor		
CC	FCTRI, or platelet derived growth factor D (PDGFD), a secreted protein		
CC	that shows homology to human vascular endothelial growth factor E and to		
CC	human PDGFs A, B and C. FCTRI RNA is present in pituitary gland tissues,		
CC	uterine microvascular endothelial cells, erythroleukaemia cells, thyroid,		
CC	small intestine, lymphocytes, adrenal gland and salivary gland. The		
CC	invention provides FcFCX and FCTRX growth factors, polypeptides and		

Query Match	100.0%	Score 370;	DB 5;	Length 370;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 370;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	MHRLLFVYTLICANFCSCRDTSATPQASIKLRLNANLRDSENHUTDLYRRDETIOVKG	60	
DB	1	MHRLLFVYTLICANFCSCRDTSATPQASIKLRLNANLRDSENHUTDLYRRDETIOVKG	60	
QY	61	NGYVQSPRPSPNSYPENLLLTWRHLSQENTRIQIOLVFNQFGLBEAENDICRYDFVEVEDIS	120	
DB	61	NGYVQSPRPSPNSYPENLLLTWRHLSQENTRIQIOLVFNQFGLBEAENDICRYDFVEVEDIS	120	
QY	121	ETSTTIRRCWGGHKEVPPRIKSRITNQIKITFKSDIYFAAKPGFKIYSLLEDFOPPAASE	180	
DB	121	ETSTTIRRCWGGHKEVPPRIKSRITNQIKITFKSDIYFAAKPGFKIYSLLEDFOPPAASE	180	
QY	181	TNWSVTSISIGSVSNPSVPDPTLIADALDKKIEPFDVEDLTXYFNPSNOEDLENNY	240	
DB	181	TNWSVTSISIGSVSNPSVPDPTLIADALDKKIEPFDVEDLTXYFNPSNOEDLENNY	240	
QY	241	LDTPRYRGRSHYDRKSKYVDLRLNDLNDAKRYSCCTPNNSYVNIIEELKLAHVFFPRCLIAQ	300	
DB	241	LDTPRYRGRSHYDRKSKYVDLRLNDLNDAKRYSCCTPNNSYVNIIEELKLAHVFFPRCLIAQ	300	
QY	301	RCGGNGCGGTYNWRSCCTNSGKTVAKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC	360	
DB	301	RCGGNGCGGTYNWRSCCTNSGKTVAKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC	360	
QY	361	DCICSSRPFR 370		
DB	361	DCICSSRPFR 370		
RESULT 12				
ABG92893				
ID	ABG92893 standard; protein; 370 AA.			
AC	ABG92893;			
XX				
DT	19-NOV-2002 (first entry)			
XX				
DE	Human VEGF-like protein zvegf 4.			
XX				
XX	VEGF: vascular endothelial growth factor; zvegf 3; human;			
KM	chromosome 4q28.3; cell proliferation; differentiation; metabolism;			
KM	migration; revascularisation; solid tumour; diabetic retinopathy;			
KM	psoriasis; rheumatoid arthritis; cancer; autoimmune disease;			
KM	inflammation; myocardial ischemia; scleroderma; fibrosis;			
KM	glomeruloclerosis; atherosclerosis; skin wound; ulcer; burn;			
KM	skin grafting; female reproductive tract disorder; chronic liver disease;			
KM	circulatory disorders; heart failure; neurodegenerative disease;			
KM	multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;			
KM	neutrite outgrowth.			
XX				
OS	Homo sapiens.			
XX				
PN	US6432673-B1.			
XX				
PD	13-AUG-2002.			
XX				

PF 07-DEC-1999; 99US-00457066.
 XX 07-DEC-1998; 98US-0111173P.
 PR 06-JUL-1999; 99US-0142576P.
 PR 21-OCT-1999; 99US-0161653P.
 PR 12-NOV-1999; 99US-0165255P.
 XX (ZYMO) ZYMOGENETICS INC.
 PI Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE,
 PI Gilbertson DG, West JW;
 DR WPI, 2002-689759/74.
 DR N-PsDB; ABS68643.
 XX Novel polypeptide, designated zvegf3 useful for treating skin wounds,
 PT ulcers, burns, skin grafting, female reproductive tract disorders,
 PT Parkinson's disease, and Alzheimer's disease.
 PS Disclosure; Col 95-98; 68pp; English.
 XX The invention relates to an isolated polypeptide, designated zvegf3 (a
 CC vascular endothelial growth factor-like protein) of 111-136 amino acid
 CC residues in length and comprises the sequence appearing as ABG92889 from
 CC amino acid residues 235-345. Also included are an isolated protein
 CC comprising a first polypeptide disulphide bonded to a second polypeptide,
 CC where each of the first and second polypeptides is from zvegf 3, and
 CC where the protein modulates cell proliferation, differentiation,
 CC metabolism or migration, the zvegf 3 encoding polynucleotides and zvegf 3
 CC expression vectors and host cells. Zvegf 3 is useful as additives in
 CC tissue adhesives for promoting revascularisation of the healing tissue,
 CC for designing molecules that antagonise semaphorin-stimulated activities,
 CC including neurite growth, cardiovascular development, cartilage and limb
 CC development, and T and B-cell function, and for imaging tumours or other
 CC sites of abnormal cell proliferation and in gene therapy applications.
 CC The proteins are useful therapeutically to stimulate tissue development
 CC or repair, or cellular differentiation or proliferation, for stimulating
 CC the growth of fibroblast or smooth muscle cells, as molecular weight
 CC standards, as reagents in assays for determining circulatory level of the
 CC protein or as standards in the analysis of cell phenotype, for
 CC identifying inhibitors of their activity which are useful for reducing
 CC the growth of solid tumours, for treating diabetic retinopathy,
 CC psoriasis, rheumatoid arthritis, various forms of cancers, autoimmune
 CC disease, inflammation, myocardial ischaemia, scleroderma, and reducing
 CC fibrosis, including scar formation, keloids, liver fibrosis, lung
 CC fibrosis (e.g. silicosis, asbestosis), kidney fibrosis (including
 CC diabetic nephropathy), glomerulosclerosis, atherosclerosis, skin wounds,
 CC ulcers, burns, skin grafting, and female reproductive tract disorders,
 CC chronic liver disease (hepatitis), cirrhosis, Reye's syndrome, Wilson's
 CC disease, circulatory disorders e.g. heart failure, hepatic or portal vein
 CC thrombosis, cardiac sclerosis, neurodegenerative diseases such as
 CC multiple sclerosis, Parkinson's disease, Alzheimer's disease, and for
 CC regenerating neurite outgrowth following strokes. The gene for human
 CC zvegf3 is located on chromosome 4q28.3. The present sequence represents
 CC zvegf 3
 XX
 SQ Sequence 370 AA;
 Query Match 100.0%; Score 370; DB 5; Length 370;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 TMNESVTSSISGVSYNSPSVTPTLIADALDKIAEPTVEDLLKYNPESWQEDLENNY 240
 DB 181 TMNESVTSSISGVSYNSPSVTPTLIADALDKIAEPTVEDLLKYNPESWQEDLENNY 240
 QY 241 LDTPRYGRSYHDRSKYVDLRLNDADAKRYSCTPRNYSVNIREBLKANVFFPRCLLVQ 300
 DB 241 LDTPRYGRSYHDRSKYVDLRLNDADAKRYSCTPRNYSVNIREBLKANVFFPRCLLVQ 300
 QY 301 RCGNCGCGCTNNMSCTCNSGKYKHEVLOFEPGHIKRGRAKTMALVDIQLDHERC 360
 DB 301 RCGNCGCGCTNNMSCTCNSGKYKHEVLOFEPGHIKRGRAKTMALVDIQLDHERC 360
 QY 361 DCICSSRPPR 370
 DB 361 DCICSSRPPR 370
 RESULT 13
 AAB47891
 ID AAB47891 standard; protein; 370 AA.
 AC AAB47891;
 XX 16-MAY-2002 (first entry)
 DT Human zvegf4.
 XX Human, mouse; zvegf4; platelet derived growth factor; PDGF;
 KM homolog; growth; bone; ligament; cartilage; proliferation; osteoblast;
 KM chondrocyte; bony defect; fracture; bone graft; implant;
 KM periodontal pocket; osteoclast; bone marrow stem cell; osteoporosis.
 XX Homo sapiens.
 OS US2002004225-A1.
 XX 10-JAN-2002.
 XX 29-MAR-2001; 2001US-00823033.
 PF 07-DEC-1998; 98US-0111173P.
 PR 06-JUL-1999; 99US-0142576P.
 PR 21-OCT-1999; 99US-0161653P.
 PR 12-NOV-1999; 99US-0165255P.
 PR 07-DEC-1999; 99US-00457066.
 PR 31-MAR-2000; 2000US-0193723P.
 XX (HART/) HART C E.
 PA (GILB/) GILBERTSON D G.
 XX Hart CE, Gilbertson DG;
 PI WPI, 2002-171026/22.
 DR Promoting growth of bone, ligament or cartilage in a mammal, involves
 PT administering to the mammal a protein which comprises growth factor
 PT domain of zvegf3 protein, a homolog of platelet-derived growth factor.
 XX Claim 8; Page 20-21, 31pp; English.
 XX This sequence represents human zvegf4. zvegf4 can be used in a
 CC composition with either human or mouse zvegf3, for promoting growth of
 CC bone, ligament or cartilage and stimulating proliferation of osteoblasts
 CC or chondrocytes in a mammal. zvegf3 is a platelet derived growth factor
 CC (PDGF) homolog. The zvegf3 protein used was preferably a dimeric protein
 CC of residues 235-345 of human zvegf3 or all of the mouse zvegf3 protein,
 CC with a delivery vehicle. The method of th invention is useful for
 CC promoting growth of bone, ligament or cartilage in a mammal, where the
 CC composition is administered at a site of a bony defect, preferably a
 CC fracture, bone graft site, implant site, or periodontal pocket, and for
 CC stimulating proliferation of osteoblasts or chondrocytes in a mammal. It
 CC is further useful for promoting proliferation of osteoblasts.

CC osteoclasts, chondrocytes or bone marrow stem cells, where the bone
 CC marrow stem cells are harvested from a patient prior to culture. The
 CC method is therefore useful for treating osteoporosis

XX
 SQ Sequence 370 AA:

Query Match 100.0%; Score 370; DB 5; Length 370;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLIFVYTLICANFSCSDTSATPOSASIKALRNANLRDSENHLLTDLYRDETIQVKG 60
 DB 1 MRLIFVYTLICANFSCSDTSATPOSASIKALRNANLRDSENHLLTDLYRDETIQVKG 60
 QY 61 NGVOSPREPNSYPRNLLTWRLHSEENTRIQLVPNOGFLGEAENDICRYDFVEVEDIS 120
 DB 61 NGVOSPREPNSYPRNLLTWRLHSEENTRIQLVPNOGFLGEAENDICRYDFVEVEDIS 120
 QY 121 ESTTIIRGWCHEKVEPRPKSRITNOIKITFKSDDFVAKPGFKIYVSLLEDFQPAASB 180
 DB 121 ESTTIIRGWCHEKVEPRPKSRITNOIKITFKSDDFVAKPGFKIYVSLLEDFQPAASB 180
 QY 181 TWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVEDLLKTFNPESQEDLENNY 240
 DB 181 TWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVEDLLKTFNPESQEDLENNY 240
 QY 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNVSVNIREELKLANVVFPPCLVQ 300
 DB 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNVSVNIREELKLANVVFPPCLVQ 300
 QY 301 RCGNGCGCGTVMNRSCITCNSGKTVKKYHEVLOFEPGHIKRGAKTMALVDIQLDHERC 360
 DB 301 RCGNGCGCGTVMNRSCITCNSGKTVKKYHEVLOFEPGHIKRGAKTMALVDIQLDHERC 360
 QY 361 DCICSSRPPR 370
 DB 361 DCICSSRPPR 370

RESULT 14
 ABB79588
 ID ABB79588 standard; protein; 370 AA.
 AC ABB79588;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human zvegf4 protein.
 XX
 DE zvegf4; human; kidney; acute tubular necrosis; nephrotropic;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= Signal_peptide
 FT Protein 19..370
 FT /label= CUB_domain+interdomain+growth_factor_domain
 FT /note= "alternatively comprises residues 24-370, 25-370,
 FT 35-370 or 52-370"
 FT Domain 180..370
 FT /label= Growth_factor_domain+interdomain
 FT Domain 246..370
 FT /label= Growth_factor_domain
 FT /note= "alternatively comprises residues 250-370 or 258-
 FT 370"
 XX
 PN WO200260467-A2.
 PD 08-AUG-2002.
 XX
 PF 26-OCT-2001, 2001WO-US050155.

XX
 XX 30-OCT-2000; 2000US-0244479P.
 PR
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Hart CE, Topouzis S;
 XX
 DR WPI: 2002-590847/63.
 DR N-PSDB; ABBN44420.
 XX
 PT Improving kidney function, or enhancing proliferation or survival of
 PT kidney tubule epithelial cells or epithelial cell precursors in a mammal
 PT comprises administering a zvegf4 protein or zvegf4 protein-encoding
 PT polynucleotide.
 PS Claim 4; Page 38-39; 45pp; English.
 XX
 CC The present sequence is the protein sequence of human vegf4, a protein
 CC which activates the alpha-alpha, alpha-beta and beta-beta forms of the
 CC platelet-derived growth factor (PDGF) receptor. Zvegf4 is structurally
 CC related to PDGF and vascular endothelial growth factor. Structural
 CC predictions suggest the polypeptide can form homomultimers or
 CC heteromultimers that act on tissues by modulating cell proliferation,
 CC migration, differentiation or metabolism. The polypeptide comprises a
 CC growth factor domain having a cysteine knot structure, and a CUB domain. A
 CC propeptide-like sequence extends from residue 180 to either residue 245,
 CC 249 or 257. Zvegf4 can thus be prepared in a variety of multimeric forms
 CC including zvegf4(19-370), zvegf4(52-370), zvegf4(246-370), zvegf4(250-
 CC 370) and zvegf4(258-370). Expression of zvegf4 polynucleotide in cultured
 CC mammalian cells results in production of a disulfide-bonded, dimeric
 CC protein. Mitogenically active protein is generated upon proteolytic
 CC processing to remove the CUB and interdomain regions. An active growth
 CC factor domain dimer can be produced directly by expressing a truncated
 CC polynucleotide. A claimed method of improving kidney function, or
 CC enhancing proliferation or survival of kidney tubule epithelial cells or
 CC epithelial cell precursors in a mammal, comprises administering a
 CC composition containing a zvegf4 protein or zvegf4 protein-encoding
 CC polynucleotide in combination with a delivery vehicle. The method is
 CC especially useful for improving kidney function in a mammal suffering
 CC from acute tubular necrosis. The zvegf4 protein is preferably a disulfide
 CC bonded dimer of 2 polypeptide chains comprising residues 258-370, 250-
 CC 370 or 246-370 of the present sequence, or a disulfide-bonded dimer of 2
 CC polypeptide chains, each chain consisting of residues x - y, where the
 CC protein is optionally glycosylated, and x is 16, 17, 18, 19, 20, 21, 22,
 CC 24, 25, 35, 52, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185,
 CC 246, 250, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262 or 263, and y
 CC is 365, 366, 367, 369 or 370
 XX
 SQ Sequence 370 AA:
 Query Match 100.0%; Score 370; DB 5; Length 370;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLIFVYTLICANFSCSDTSATPOSASIKALRNANLRDSENHLLTDLYRDETIQVKG 60
 DB 1 MRLIFVYTLICANFSCSDTSATPOSASIKALRNANLRDSENHLLTDLYRDETIQVKG 60
 QY 61 NGVOSPREPNSYPRNLLTWRLHSEENTRIQLVPNOGFLGEAENDICRYDFVEVEDIS 120
 DB 61 NGVOSPREPNSYPRNLLTWRLHSEENTRIQLVPNOGFLGEAENDICRYDFVEVEDIS 120
 QY 121 ESTTIIRGWCHEKVEPRPKSRITNOIKITFKSDDFVAKPGFKIYVSLLEDFQPAASB 180
 DB 121 ESTTIIRGWCHEKVEPRPKSRITNOIKITFKSDDFVAKPGFKIYVSLLEDFQPAASB 180
 QY 181 TWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVEDLLKTFNPESQEDLENNY 240
 DB 181 TWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVEDLLKTFNPESQEDLENNY 240
 QY 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNVSVNIREELKLANVVFPPCLVQ 300
 DB 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNVSVNIREELKLANVVFPPCLVQ 300

PT diabetes, asthma, psoriasis, Parkinson's and Alzheimer's.
 XX
 XX Claim 11: Page 389-390; 238pp; English.
 CC The invention relates to an isolated nucleic acid molecule which encodes
 CC a human secreted protein. The sequences are useful for diagnosing or
 CC diagnosing a susceptibility to a pathological condition in a subject
 CC comprising determining the presence or absence of a mutation in the DNA
 CC or expression of the protein. The sequences are useful for identifying a
 CC binding partner to the protein comprising contacting the protein with a
 CC binding partner and determining whether the binding partner effects an
 CC activity. The DNA and protein sequences are used for preventing, treating
 CC or ameliorating a medical condition such as an autoimmune disease (e.g.
 CC multiple sclerosis, myasthenia gravis), blood coagulation disorders (e.g.
 CC afibrinogenemia, haemophilia), blood platelet disorders (e.g.
 CC thrombocytopenia), hyperproliferative disorders (e.g. sarcoidosis, Sezary
 CC syndrome), neurodegenerative disorders (e.g. Alzheimer's disease,
 CC Parkinson's disease), renal disorders (e.g. renal vein thrombosis, kidney
 CC infarction), cardiovascular disorders (e.g. cardiac arrest,
 CC pericarditis), vascular disorders (e.g. aneurysm, ischaemia), respiratory
 CC disorders (e.g. tonsillitis, laryngitis), endocrine disorders (e.g.
 CC acromegaly, thyrotoxicosis), reproductive disorders (gonorrhea,
 CC anorchia), gastrointestinal disorders (e.g. gastroenteritis, pyloric
 CC stenosis), infectious diseases (e.g. polio, rubella) and cancer.
 CC Sequences ABG76569-ABG76616 represent human secreted proteins of the
 CC invention
 XX
 SQ Sequence 370 AA:
 Query Match 100.0%; Score 370; DB 5; Length 370;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MHRLLFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLDYRRDETTQVKG 60
 DB 1 MHRLLFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLDYRRDETTQVKG 60
 QY 61 NGVQSPRPFPNSYPRLNLLTWRLHSEOENTRIQLVFNQGLBEAENDICRYDVEVEDIS 120
 DB 61 NGVQSPRPFPNSYPRLNLLTWRLHSEOENTRIQLVFNQGLBEAENDICRYDVEVEDIS 120
 QY 121 ESTTIIRGRWCGHKEVPPRIKSRITNOIKITPKSDDFVAKPGFKIYYSLLLEDFQPAASE 180
 DB 121 ESTTIIRGRWCGHKEVPPRIKSRITNOIKITPKSDDFVAKPGFKIYYSLLLEDFQPAASE 180
 QY 181 TNWESVTSSISGVSYNSPSVTPTLLIADALDKKIAEFDVIEDLLKYNFESQEDLENNY 240
 DB 181 TNWESVTSSISGVSYNSPSVTPTLLIADALDKKIAEFDVIEDLLKYNFESQEDLENNY 240
 QY 241 LDTPRRGRSYHNRKSKVDRLNDADAKRYSCTPRPNYSVINIRELKLAVVFPRLCLVQ 300
 DB 241 LDTPRRGRSYHNRKSKVDRLNDADAKRYSCTPRPNYSVINIRELKLAVVFPRLCLVQ 300
 QY 301 RCGNCGCGTVMNRSCCTCNSGKTIVKKYHEVLQEPFGHKKRGRAKTMALVDIQLDHHERC 360
 DB 301 RCGNCGCGTVMNRSCCTCNSGKTIVKKYHEVLQEPFGHKKRGRAKTMALVDIQLDHHERC 360
 QY 361 DCICSSRPPR 370
 DB 361 DCICSSRPPR 370
 RESULT 17
 ABG64733 ID ABG64733 standard; protein; 370 AA.
 XX AC ABG64733;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Human albumin fusion protein #1408.
 XX
 KW Albumin fusion protein; therapeutic protein X; human albumin; HA;

KW human serum albumin; HSA; cancer; reproductive disorder;
 KW digestive disorder; immune disorder; endocrine disorder;
 KW haematopoietic disorder; neural disorder; connective disorder;
 KW cytostatic; antifertility; antiinflammatory; anticler;
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nocotropic;
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
 KW osteopathic; antiarthritic.
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200177137-A1.
 PD 18-OCT-2001.
 PF 12-APR-2001; 2001WO-US011988.
 PF 12-APR-2000; 2000US-0229358P.
 PR 25-APR-2000; 2000US-0199384P.
 PR 21-DEC-2000; 2000US-0256931P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Haseltine WA;
 XX
 DR WPI, 2002-010886/01.
 PT New fusion protein for treating disease e.g. diabetes comprises an
 PT albumin fused to a therapeutic protein.
 XX
 PS Claim 1: Page 1459-1460; 2102pp; English.
 XX
 CC The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein X and human albumin (HA, also known as human serum
 CC albumin, HSA). The proteins are useful for treating a disease or disorder
 CC that may be modulated by therapeutic protein X. The albumin extends the
 CC shelf-life of protein X, and may increase its biological in vitro/in vivo
 CC activity. The protein is useful for treating and diagnosing disorders
 CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
 CC disease, ulcerative colitis), immune disorders (e.g. acquired
 CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
 CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
 CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
 CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
 CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
 XX
 SQ Sequence 370 AA:
 Query Match 100.0%; Score 370; DB 5; Length 370;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MHRLLFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLDYRRDETTQVKG 60
 DB 1 MHRLLFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLDYRRDETTQVKG 60
 QY 61 NGVQSPRPFPNSYPRLNLLTWRLHSEOENTRIQLVFNQGLBEAENDICRYDVEVEDIS 120
 DB 61 NGVQSPRPFPNSYPRLNLLTWRLHSEOENTRIQLVFNQGLBEAENDICRYDVEVEDIS 120
 QY 121 ESTTIIRGRWCGHKEVPPRIKSRITNOIKITPKSDDFVAKPGFKIYYSLLLEDFQPAASE 180
 DB 121 ESTTIIRGRWCGHKEVPPRIKSRITNOIKITPKSDDFVAKPGFKIYYSLLLEDFQPAASE 180
 QY 181 TNWESVTSSISGVSYNSPSVTPTLLIADALDKKIAEFDVIEDLLKYNFESQEDLENNY 240
 DB 181 TNWESVTSSISGVSYNSPSVTPTLLIADALDKKIAEFDVIEDLLKYNFESQEDLENNY 240
 QY 241 LDTPRRGRSYHNRKSKVDRLNDADAKRYSCTPRPNYSVINIRELKLAVVFPRLCLVQ 300
 DB 241 LDTPRRGRSYHNRKSKVDRLNDADAKRYSCTPRPNYSVINIRELKLAVVFPRLCLVQ 300
 QY 301 RCGNCGCGTVMNRSCCTCNSGKTIVKKYHEVLQEPFGHKKRGRAKTMALVDIQLDHHERC 360
 DB 301 RCGNCGCGTVMNRSCCTCNSGKTIVKKYHEVLQEPFGHKKRGRAKTMALVDIQLDHHERC 360


```

FT      /note="Specifically claimed in claim 5"
FT      Region
FT      250..370
FT      /note="Specifically claimed in claim 7"
FT      Region
FT      250..370
FT      /note="Specifically claimed in claim 2"
FT      258..370
FT      /note="Specifically claimed in claim 1"
XX      US6495668-B1.
XX
XX      17-DEC-2002.
XX
XX      03-MAY-2000; 2000US-00564595.
XX
XX      03-MAY-1999; 99US-0132250P.
XX      10-NOV-1999; 99US-0164463P.
XX      04-FEB-2000; 2000US-0180169P.
XX
XX      (ZYMO ) ZYMOGENETICS INC.
XX
XX      Gilbert T, Hart CE, Shepard PO, Gilbertson DG;
XX      WPI, 2003-352153/33.
XX      N-PSDB; ACA64109.
XX
XX      Isolated growth factor analogue ZVEGF4 proteins for pharmaceutical
XX      composition as, e.g. therapeutic agents, diagnostic agents, and research
XX      tools and reagents, includes polypeptides from amino acid residues.
XX
XX      Claim 1; Col 71-72; 67pp; English.
XX
XX      The invention relates to an isolated protein comprising a first
XX      and second polypeptide disulphide-bonded to a second polypeptide. The first and
XX      second polypeptides are from 113-138 amino acid residues and comprises
XX      258-370 amino acid residues of human growth factor homologue ZVEGF4. The
XX      protein stimulates proliferation, differentiation, or migration of
XX      mesenchymal cells and may modulate activities mediated by cell surface
XX      semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-
XX      semaphorin interactions which may be of use in neurite growth,
XX      cardiovascular development, cartilage and limb development, T- and B-cell
XX      functions as well as treating rheumatoid arthritis, various forms of
XX      cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas,
XX      ischemic events, neuropathies, acute nerve damage, central nervous
XX      system diseases and peripheral nervous system diseases including stroke.
XX      The isolated protein is also used for a pharmaceutical composition as
XX      therapeutic agents, diagnostic agents, and research tools and reagents.
XX      It can be used in the study and regulation of cell and tissue
XX      development, as components of cell culture media. The proteins can form
XX      homooligomers or heterooligomers that act on tissues to control organ
XX      development by modulating cell proliferation, migration, differentiation,
XX      or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3
XX      -23.1. The present sequence represents human ZVEGF4
XX
XX      Sequence 370 AA:
XX
Query Match      100.0%; Score 370; DB 6; Length 370;
Best Local Similarity 100.0%; Pred. No.0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db      181 TWNESVTSSISGVSYNSPSVTDEPTLIADALDKKIAEDTVEDLLKYNFESMOEDLENNY 240
Qy      241 LDPFRGRSSYHDRKSKVLDLRNDPAKRYSCPRPYSVINIRELKLAVVFPRLCLVO 300
Db      241 LDPFRGRSSYHDRKSKVLDLRNDPAKRYSCPRPYSVINIRELKLAVVFPRLCLVO 300
Qy      301 RCGNCGCTVWVRSCCTCNSGKTVKKYHEVLOFEPGHIKRRGRAKTMAVLVDLDHHERC 360
Db      301 RCGNCGCTVWVRSCCTCNSGKTVKKYHEVLOFEPGHIKRRGRAKTMAVLVDLDHHERC 360
Qy      361 DCICSSRPPR 370
Db      361 DCICSSRPPR 370

RESULT 20
ID      ABG76397 standard; protein; 370 AA.
XX      ABG76397;
XX
XX      AC      ABG76397;
XX      DT      22-MAY-2003 (first entry)
XX      DE      Human growth factor homologue, zvegf4.
XX
XX      KW      Human; growth factor homologue; zvegf4; fibroblast; smooth muscle cell;
XX      cell-surface platelet-derived growth factor alpha receptor; PDGF;
XX      full-thickness skin wound; female reproductive tract; duodenal ulcer;
XX      prolonged bleeding; periodontal disease; tissue adhesive; liver damage;
XX      revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis;
XX      chronic active hepatitis; hepatic chronic passive congestion; stroke;
XX      central haemorrhagic necrosis; hepatic vein thrombosis; jaecemia;
XX      portal vein thrombosis; cardiac sclerosis; new vessel formation;
XX      endothelial precursor stem cell; neovascularisation; wound healing;
XX      organ transplant; tissue grafting; peripheral neuropathy; spinal cord;
XX      sensory neurite outgrowth; brain damage; head injury; paralysis;
XX      spinal injury; neurodegenerative disease; diabetic retinopathy;
XX      psoriasis; arthritis; scleroderma; keloid; liver fibrosis; psoriasis;
XX      lung fibrosis; kidney fibrosis; glomerulosclerosis; cancer;
XX      proliferative vascular disorder; rheumatoid arthritis; vasculogenesis;
XX      inflammatory disorder; rheumatoid arthritis; vasculogenesis;
XX      angiogenesis; nervous system disorder; cytostatic; hepatocytic;
XX      vulnary; tranquilliser; cerebroprotective; neuroprotective; nootropic;
XX      ophthalmological; dermatological; coagulant; cardiant.
XX
XX      OS      Homo sapiens.
XX
XX      PN      US200217193-A1.
XX
XX      PD      28-NOV-2002.
XX
XX      PF      02-MAY-2002; 2002US-00139583.
XX
XX      PR      07-DEC-1998; 98US-011173P.
XX      06-JUL-1999; 99US-0142576P.
XX      21-OCT-1999; 99US-0161651P.
XX      12-NOV-1999; 99US-0165255P.
XX      07-DEC-1999; 99US-00457066.
XX
XX      PA      (ZYMO ) ZYMOGENETICS INC.
XX
XX      PI      Gao Z, Hart CE, Piddington CS, Shepard PO, Shoemaker KE;
XX      Gilbertson DG, West JW;
XX      WPI, 2003-328465/31.
XX      N-PSDB; ABX93177.
XX
XX      PT      New isolated zvegf3 polypeptide, useful for treating cancer, Alzheimer's
XX      disease, Parkinson's disease, chronic active hepatitis, hepatic vein
XX      thrombosis, comprises growth factor domain and CUB domain.
XX      Disclosure; Page 51-52; 73pp; English.
XX

```

CC The present invention relates to the isolation of a growth factor
CC homologue referred to as zvegf3, and the polynucleotide sequence encoding
CC it. The zvegf3 polypeptide is useful for stimulating the growth of
CC fibroblasts or smooth muscle cells, or for activating a cell-surface
CC platelet-derived growth factor (PDGF) alpha receptor. The zvegf3
CC polypeptide is useful as a PDGF alpha receptor agonist and thus is useful
CC for treating full-thickness skin wounds, female reproductive tract and
CC prolonged bleeding, periodontal disease, damaged liver tissue, and
CC duodenal ulcers. The polypeptide is also useful as an additive in tissue
CC adhesives for promoting revascularisation of healing tissue. The zvegf3
CC polypeptide is also useful for treating liver damage including damage due
CC to liver disease, chronic active hepatitis, hepatic chronic passive
CC congestion (CCP), central haemorrhagic necrosis (CHN), hepatic vein
CC thrombosis, portal vein thrombosis, cardiac sclerosis, and many types of
CC cirrhosis. The polypeptide is useful for enhancing expansion and
CC stabilisation of endothelial precursor stem cells, creating and
CC including new vessel formation in areas requiring neovascularisation,
CC including areas of ischemia, organ transplants, wound healing, and
CC tissue grafting. It may be used for treating peripheral neuropathies by
CC increasing spinal cord and sensory neurite outgrowth, and as part of
CC therapeutic treatment for the regeneration of neurite outgrowths
CC following strokes, brain damage caused by head injuries, and paralysis
CC caused by spinal injuries. Application may also be made in treating
CC neurodegenerative diseases (e.g. multiple sclerosis, Alzheimer's disease,
CC Parkinson's disease), diabetic retinopathy, psoriasis, arthritis,
CC scleroderma, and reducing fibrosis, keloids, liver fibrosis, lung
CC fibrosis, kidney fibrosis, and glomerulosclerosis. An antibody that binds
CC zvegf3 is useful for blocking the mitogenic, chemocactic, or angiogenic
CC effects of zvegf3, and for treating proliferative vascular disorders,
CC ocular neovascularisation, inflammatory disorders, rheumatoid arthritis,
CC psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis,
CC and diseases of the nervous system. The present sequence represents human
CC zvegf4
XX

SQ Sequence 370 AA:

Query Match 100.0%; Score 370; DB 6; Length 370;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVTLICANCSGCDTATPOSASIKALRNANLRDSSNHLTDYRDETIQVKG 60
DB 1 MHRLLFVTLICANCSGCDTATPOSASIKALRNANLRDSSNHLTDYRDETIQVKG 60
QY 61 NGYVSPRPFPNSYPENLLTWRLHSQENTRIQLVDFNCGLEAEANDICRYFVEVEDIS 120
DB 61 NGYVSPRPFPNSYPENLLTWRLHSQENTRIQLVDFNCGLEAEANDICRYFVEVEDIS 120
QY 121 ESTTIRGRWCGHKEVPRPKIRTNQIKITFKSSDYFVAKPGFKIYSLDEPQPAASE 180
DB 121 ESTTIRGRWCGHKEVPRPKIRTNQIKITFKSSDYFVAKPGFKIYSLDEPQPAASE 180
QY 121 TWNEVTSISGSVNSPSVPTDPTLIADLDKKIEFDVDELLKYFNPESQOELENNY 240
DB 121 TWNEVTSISGSVNSPSVPTDPTLIADLDKKIEFDVDELLKYFNPESQOELENNY 240
QY 241 LDTPEYRGHSYHDRSKYVDLRLNDAKKYSCTPNANYSNIEBEKLANVFFPCLVLQ 300
DB 241 LDTPEYRGHSYHDRSKYVDLRLNDAKKYSCTPNANYSNIEBEKLANVFFPCLVLQ 300
QY 301 RCGNCGCGCTVNRSCCTNSGKTVKKYHEVLOPEFGHKKRGRAKTMALVDIQLDHERC 360
DB 301 RCGNCGCGCTVNRSCCTNSGKTVKKYHEVLOPEFGHKKRGRAKTMALVDIQLDHERC 360
QY 361 DCTCSSRPR 370
DB 361 DCTCSSRPR 370

RESULT 21
ABB80134
ID ABB80134 standard; protein; 370 AA.
XX

AC ABB80134;
XX
DT 27-JUN-2003 (first entry)
XX
DE PDGF-D.
XX
XX Nervous system; platelet-derived growth factor; PDGF; psychosis;
KW Vascular endothelial growth factor; VEGF; neural; stem cell; neuro;
KW progenitor cell; neurodegeneration; ischemia; neurological trauma;
KW neuropsychiatry; learning; Parkinson's disease; Huntington's disease;
KW Amyotrophic lateral Sclerosis; spinal ischemia; ischemic stroke;
KW spinal cord injury; cancer-related; schizophrenia; Alzheimer's disease;
KW depression; anxiety; phobia; stress; cognitive function; aggression;
KW drug; alcohol; abuse; obsessive compulsive behaviour; proliferation;
KW seasonal mood disorder; personality disorder; cerebral palsy;
KW multi-infarct; dementia; Lewy body; age related; geriatric; growth;
KW epilepsy; brain injury; multiple sclerosis; autism; differentiation;
KW attention deficit disorder; narcolepsy.
XX
OS Homo sapiens.
XX
PN WO2003024478-A1.
XX
XX 27-MAR-2003.
PD
PF 19-SEP-2002; 2002WO-IB003998.
XX
PR 19-SEP-2001; 2001US-0323381P.
XX
PR 28-SEP-2001; 2001US-0326044P.
XX
PA (NEUR-) NEURONOVA AB.
XX
PI Delfant K, Janson AM, Kuhn GH, Plate K, Schanzer A, Wachs F;
PI Zhao M;
XX
XX WPI: 2003-354563/33.
XX
DR N-PSDB; AB080246.
XX
PT Use of platelet-derived growth factor, vascular endothelial growth
PT factor, or their modulators for modulating neural stem cell or neural
PT progenitor cell activity, particularly for treating e.g. Alzheimer's,
PT ischemia or stroke.
XX
PS Disclosure; Page 23; 119pp; English.
XX
XX The sequences given in ABB80131-35 show proteins which may be used in the
XX method of the invention for alleviating or reducing a symptom of a
XX disease or disorder of the nervous system. The method comprises
XX administering platelet-derived growth factor (PDGF), vascular endothelial
XX growth factor (VEGF), a combination of PDGF and VEGF, or a PDGF or VEGF
XX agonist, to a patient in order to modulate neural stem cell or neural
XX progenitor cell activity in vivo. The method is useful for alleviating or
XX reducing the symptoms of a disease or disorder of the nervous system,
XX e.g. neurodegenerative disorders, neural stem cell disorders, neural
XX progenitor disorders, ischemic disorders, neurological traumas,
XX affective disorders, neuropsychiatric disorders or learning and memory
XX disorders. In particular, the method is useful for alleviating or
XX treating Parkinson's disease and disorders, Huntington's disease,
XX Alzheimer's disease, Amyotrophic lateral Sclerosis, spinal ischemia,
XX ischemic stroke, spinal cord injury or cancer-related brain/spinal cord
XX injury, schizophrenia and other psychoses, depression, bipolar
XX depression/disorder, anxiety syndromes/disorders, phobias, stress and
XX related syndromes, cognitive function disorders, aggression, drug and
XX alcohol abuse, obsessive compulsive behaviour syndromes, seasonal mood
XX disorder, borderline personality disorder, cerebral palsy, life style
XX drug, multi-infarct dementia, Lewy body dementia, age related/geriatric
XX dementia, epilepsy and injury related to epilepsy, spinal cord injury,
XX brain injury, trauma related brain/spinal cord injury, infection and
XX treatment related brain/spinal cord tissue injury, environmental toxin
XX inflammation related brain/spinal cord injury, environmental toxin
XX related brain/spinal cord injury, multiple sclerosis, autism, attention
XX deficit disorders, narcolepsy or sleep disorders. The PDGF and/or VEGF,
XX is useful in the manufacture of a medicament for alleviating or treating

CC these diseases or disorders, accelerating growth of neural stem cells or
CC neural progenitor cells, or inducing proliferation or differentiation of
CC these cells

XX SQ Sequence 370 AA:

Query Match 100.0%; Score 370; DB 6; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYLLICANFSCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
DB 1 MHRLLFVYLLICANFSCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
QY 61 NGVQSPRPFPNSYPRLNLLTWRLHSEENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
DB 61 NGVQSPRPFPNSYPRLNLLTWRLHSEENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
QY 121 ETSIIIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEQPAASE 180
DB 121 ETSIIIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEQPAASE 180
QY 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVEDLLKTFNPESWQEDLENNY 240
DB 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVEDLLKTFNPESWQEDLENNY 240
QY 241 LDPFRYGRSYHDKRSKVDLRLNDDAKRYSCTPRNVSVNIRELKLAVVFFPRCLLVQ 300
DB 241 LDPFRYGRSYHDKRSKVDLRLNDDAKRYSCTPRNVSVNIRELKLAVVFFPRCLLVQ 300
QY 301 RCGNCGCGTVMWRSCTCNSGKTVMKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERC 360
DB 301 RCGNCGCGTVMWRSCTCNSGKTVMKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 22

ABR43944
ID ABR43944 standard; protein; 370 AA.

XX AC ABR43944;

XX DT 11-AUG-2003 (first entry)

XX DE Human PDGF-D polypeptide.

XX KW Platelet-derived growth factor-D; PDGF-D; osteopathic; vulnary; bone;
XX connective tissue; human.

XX OS Homo sapiens.

XX FT Key Location/Qualifiers
258..365

XX FT Domain /note="core growth factor domain"

XX PN WO2003033677-A2.

XX PD 24-APR-2003.

XX PF 18-OCT-2002; 2002WO-US033563.

XX PR 19-OCT-2001; 2001US-0346117P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Moore MD, Fox BA;

XX DR WPI; 2003-421322/39.

XX DR N-PSDB; ACC47941.

PT New protein consisting of two platelet-derived growth factor-D
PT polypeptide chains, useful for stimulating the production of bone and/or
PT connective tissue in both humans and animals, e.g. in treating fractures
PT or osteoporosis.

XX Claim 1; Page 34-37; 47pp; English.

CC The invention relates to a protein consisting of two platelet-derived
CC growth factor-D (PDGF-D) polypeptide chains. The protein is useful in
CC enhanced production of PDGF-D growth factor domain dimers. It may be used
CC to stimulate production of bone and/or connective tissue in both humans
CC and animals, such as in cases of fractures, bone grafts, implants, repair
CC of bony defects arising from surgery, surgical reconstruction following
CC traumatic injury, repair of hereditary or other physical abnormalities,
CC or in treatment of osteoporosis. The present sequence represents a human
CC PDGF-D polypeptide

XX SQ Sequence 370 AA:

Query Match 100.0%; Score 370; DB 6; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYLLICANFSCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
DB 1 MHRLLFVYLLICANFSCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
QY 61 NGVQSPRPFPNSYPRLNLLTWRLHSEENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
DB 61 NGVQSPRPFPNSYPRLNLLTWRLHSEENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
QY 121 ETSIIIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEQPAASE 180
DB 121 ETSIIIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEQPAASE 180
QY 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVEDLLKTFNPESWQEDLENNY 240
DB 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVEDLLKTFNPESWQEDLENNY 240
QY 241 LDPFRYGRSYHDKRSKVDLRLNDDAKRYSCTPRNVSVNIRELKLAVVFFPRCLLVQ 300
DB 241 LDPFRYGRSYHDKRSKVDLRLNDDAKRYSCTPRNVSVNIRELKLAVVFFPRCLLVQ 300
QY 301 RCGNCGCGTVMWRSCTCNSGKTVMKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERC 360
DB 301 RCGNCGCGTVMWRSCTCNSGKTVMKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 23

AAE38476
ID AAE38476 standard; protein; 370 AA.

XX AC AAE38476;

XX DT 20-NOV-2003 (first entry)

XX DE Human platelet derived growth factor (PDGF-D).

XX KW Human; platelet-derived growth factor-D; PDGF-D; bone graft; osteopathic;
XX radiation-induced osteonecrosis; periodontal disease; protein therapy;
XX joint injury; osteoporosis; bone loss; fracture; bone healing.

XX OS Homo sapiens.

XX FT Key

XX FT Region Location/Qualifiers
1..18

XX FT Domain /note="Secretory peptide"
52..179
/note="CUB domain"

FT	Region	180..245
FT	/note= "Propeptide-like sequence"	
FT	Cleavage-site	245
FT	/note= "Monobasic site"	
FT	Domain	246..370
FT	/note= "PDGF-D growth factor domain"	
FT	Cleavage-site	249
FT	/note= "Monobasic site"	
FT	Cleavage-site	254..257
FT	/note= "Furin-like protease cleavage site"	
FT	Cleavage-site	254..255
FT	/note= "Dibasic site"	
XX		
PN	WO2003068802-A2.	
XX		
PD	21-AUG-2003.	
XX		
PF	11-FEB-2003; 2003WO-US004213.	
XX		
PR	11-FEB-2002; 2002US-0355882P.	
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	Fox BA, Moore MD, Swiderex KM, Birks CW;	
XX		
DR	WPI; 2003-646473/61.	
DR	N-PsDB; AAD58378.	
PT	New fusion protein comprising a first platelet-derived growth factor-D	
PT	(PDGF-D) domain, a linker, and a second PDGF-D domain polypeptides,	
PT	useful for stimulating the production of bone and/or connective tissue.	
PS	Claim 1; Page 35-36; 50pp; English.	
XX		
CC	The invention relates to a fusion protein comprising, from amino to	
CC	carboxyl terminus, a first platelet-derived growth factor-D (PDGF-D)	
CC	domain polypeptide, a linker polypeptide, and a second PDGF-D domain	
CC	polypeptide. The fusion proteins are useful for stimulating the	
CC	production of bone and/or connective tissue in both human and non-human	
CC	animals. The fusion proteins are specifically useful in non-union	
CC	fractures and fractures in patients with compromised healing, bone	
CC	grafts, bone healing following radiation-induced osteonecrosis, implants,	
CC	or treatment of periodontal disease, joint injuries, osteoporosis or	
CC	other conditions characterised by increased bone loss or decreased bone	
CC	formation. The invention is useful in protein therapy. The present	
CC	sequence is human platelet derived growth factor (PDGF-D). PDGF-D is	
CC	known as zvegfa	
XX		
SQ	Sequence 370 AA;	
	Query Match 100.0%; Score 370; DB 7; Length 370;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 MHRLIFVTTLLICANFCSCRDTSATQSASIKALRNANNLRBDSNHLTDLRDEDTIQVGK 60	
Dh	1 MHRLIFVTTLLICANFCSCRDTSATQSASIKALRNANNLRBDSNHLTDLRDEDTIQVGK 60	
OY	61 NGVGSPPFPNSYPENLLLTWRHLSHOENRIQLVFDNOGFLGEAENDICRYVFVEVEDIS 120	
Dh	61 NGVGSPPFPNSYPENLLLTWRHLSHOENRIQLVFDNOGFLGEAENDICRYVFVEVEDIS 120	
OY	121 ETSITIRGRWCCHKVPPIRKSRTNQIKITFFKSDDYFYAKPKFKIYSLIEDPQPAAASE 180	
Dh	121 ETSITIRGRWCCHKVPPIRKSRTNQIKITFFKSDDYFYAKPKFKIYSLIEDPQPAAASE 180	
OY	181 TNMESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLTKYFNESNQEDLENNY 240	
Dh	181 TNMESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLTKYFNESNQEDLENNY 240	
OY	241 LDPTRYRRGRSHYDRSKSYVDLDLNDARKYSCTPNKYSNINIELKLNAVVFPPCLVQ 300	
Dh	241 LDPTRYRRGRSHYDRSKSYVDLDLNDARKYSCTPNKYSNINIELKLNAVVFPPCLVQ 300	

Oy	301	RCGNGCGCTTWNRSCTCNSGKTVKKYKHEVLQEPFHRRGRAKMALVDIQLDHHERC	360
Db	301	RCGNGCGCTTWNRSCTCNSGKTVKKYKHEVLQEPGHKRRGRAKMALVDIQLDHHERC	360
Oy	361	DCICSSRPPR	370
Db	361	DCICSSRPPR	370
RESULT 24			
ARM02697	ABM02697	strand; protein; 370 AA.	
XX	ABM02697;		
XX	11-MAR-2004	(first entry)	
XX	Human zvegfa protein.		
XX	Therapy; osteoporosis; injury; surgery; tumour; ulceration; infection;		
KW	congenital defect; human.		
OS	Homo sapiens.		
XX			
XX	Key	Location/Qualifiers	
FT	Domain	19..370	
FT		/note="Cub domain + interdomain region + growth factor	
FT	Domain	19..257	
FT		/note="Cub domain + interdomain region"	
FT	Domain	19..179	
FT		/note="Cub domain"	
FT	Domain	180..370	
FT		/note="Growth factor domain + interdomain region"	
FT	Domain	250..370	
FT		/note="Growth factor domain"	
XX	US2003105015-A1.		
XX	05-JUN-2003.		
XX	23-AUG-2002;	2002US-00226559.	
XX	03-MAY-1999;	99US-0133250P.	
PR	10-NOV-1999;	99US-0164463P.	
PR	04-FEB-2000;	2000US-0180169P.	
PR	31-MAR-2000;	2000US-00540224.	
XX			
PA	(ZYMO) ZYMOGENETICS INC.		
XX			
PI	Gilbertson DG, Hart CE;		
XX	WPI: 2003-874621/81.		
DR	N-PSDB; AAD64615.		
PT	Method for promoting growth of bones, ligaments and cartilages in mammal,		
PT	involves administering composition containing zvegfa in vehicle.		
XX	Claim 15; SEQ ID NO 2; OGP; English.		
XX			
XX	The present invention relates to a method for promoting growth of bones,		
CC	ligaments and cartilages in a mammal. The invention is useful for		
CC	treating osteoporosis such as age related osteoporosis, post-menopausal		
CC	osteoporosis, glucocorticoid induced osteoporosis and disuse		
CC	osteoporosis. The invention is also useful in treating bony defects due		
CC	to injury, surgery, tumour removal, ulceration, infection or other		
CC	congenital defects. The present sequence is human zvegfa protein		
XX			
XX	Sequence 370 AA;		
XX			
Query Match	100.0%;	Score 370;	DB 7; Length 370;
Best local Similarity	100.0%;	Pred. No. 0;	

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLIFVYLLICANFCSCRDTSATPOSASIKALRNANLRDSDNHLTDLYRDETIQVNG 60
 DB 1 MRLIFVYLLICANFCSCRDTSATPOSASIKALRNANLRDSDNHLTDLYRDETIQVNG 60

QY 61 NGVOSPREPNSEYPRNLLTWRLHSEQENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120
 DB 61 NGVOSPREPNSEYPRNLLTWRLHSEQENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120

QY 121 EFTSTIIRGRWCGHKEVPPRIKSRTNQIKITPKSDDYFVAKPGFKIYSLLEDFQPAASE 180
 DB 121 EFTSTIIRGRWCGHKEVPPRIKSRTNQIKITPKSDDYFVAKPGFKIYSLLEDFQPAASE 180

QY 181 TWMEVSTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVEDLKYFNESWQEDLENNY 240
 DB 181 TWMEVSTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVEDLKYFNESWQEDLENNY 240

QY 241 LDTPRYGRSYHDRKSKVDLDRNDADAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300
 DB 241 LDTPRYGRSYHDRKSKVDLDRNDADAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300

QY 301 RCGNGCGCTVWNRSCCTNSGKTVKKYHEVLQFEFGHIKRRGRAKTMALVDIQLDHHERC 360
 DB 301 RCGNGCGCTVWNRSCCTNSGKTVKKYHEVLQFEFGHIKRRGRAKTMALVDIQLDHHERC 360

QY 361 DCICSSRPPR 370
 DB 361 DCICSSRPPR 370

RESULT 25
 ADG47746
 ID ADG47746 standard; protein; 370 AA.
 XX
 AC ADG47746;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human zvegfg3 related protein.
 XX
 KW Vulnerary; dermatological; wound healing; proliferation; zvegfg3.; human.
 XX
 OS Homo sapiens.
 XX
 FN US628050-B1.
 XX
 PD 04-MAR-2003.
 XX
 PF 06-NOV-2000; 2000US-00706968.
 XX
 PR 07-DEC-1998; 98US-011173P.
 PR 06-JUL-1999; 99US-0142576P.
 PR 21-OCT-1999; 99US-016153P.
 PR 12-NOV-1999; 99US-016525P.
 PR 07-DEC-1999; 99US-00457066.
 PR 31-MAR-2000; 2000US-00541752.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KB;
 PI Gilbertson DG, West JW;
 XX
 DR WPI; 2003-370630/35.
 DR N-PSDB; ADG47745.
 XX
 PT Promoting wound healing or proliferation of fibroblasts or smooth muscle
 PT cells in a mammal, by administering a polypeptide comprising growth
 PT factor domain of human growth factor homolog polypeptide, zvegfg3.
 PS Disclosure; SEQ ID NO 37; 69pp; English.
 CC The present invention relates to a method of promoting wound healing.

CC especially a dermal wound and for promoting proliferation of fibroblasts
 CC or smooth muscle cells in a mammal, by administering a polypeptide
 CC comprising growth factor domain of human growth factor homolog
 CC polypeptide, zvegfg3. The present sequence is human zvegfg3 related
 CC protein.
 CC

SQ Sequence 370 AA;

Query Match 100.0%; Score 370; DB 7; Length 370;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLIFVYLLICANFCSCRDTSATPOSASIKALRNANLRDSDNHLTDLYRDETIQVNG 60
 DB 1 MRLIFVYLLICANFCSCRDTSATPOSASIKALRNANLRDSDNHLTDLYRDETIQVNG 60

QY 61 NGVOSPREPNSEYPRNLLTWRLHSEQENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120
 DB 61 NGVOSPREPNSEYPRNLLTWRLHSEQENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120

QY 121 EFTSTIIRGRWCGHKEVPPRIKSRTNQIKITPKSDDYFVAKPGFKIYSLLEDFQPAASE 180
 DB 121 EFTSTIIRGRWCGHKEVPPRIKSRTNQIKITPKSDDYFVAKPGFKIYSLLEDFQPAASE 180

QY 181 TWMEVSTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVEDLKYFNESWQEDLENNY 240
 DB 181 TWMEVSTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVEDLKYFNESWQEDLENNY 240

QY 241 LDTPRYGRSYHDRKSKVDLDRNDADAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300
 DB 241 LDTPRYGRSYHDRKSKVDLDRNDADAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300

QY 301 RCGNGCGCTVWNRSCCTNSGKTVKKYHEVLQFEFGHIKRRGRAKTMALVDIQLDHHERC 360
 DB 301 RCGNGCGCTVWNRSCCTNSGKTVKKYHEVLQFEFGHIKRRGRAKTMALVDIQLDHHERC 360

QY 361 DCICSSRPPR 370
 DB 361 DCICSSRPPR 370

Search completed: November 10, 2005, 09:43:52
 Job time : 167 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:37:22 : Search time 43 Seconds
(without alignments)
642.329 Million cell updates/sec

Title: US-10-606-055-2
Perfect score: 370
Sequence: 1 MHRLLFVYTLICANFCSCRD.....DIQLDHERCICSSRPPR 370

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 5

Total number of hits satisfying chosen parameters: 14506

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6C_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	100.0	370	4	US-09-457-066-37
2	370	100.0	370	4	US-09-540-224-2
3	370	100.0	370	4	US-09-564-595D-2
4	370	100.0	370	4	US-09-706-968-37
5	370	100.0	370	4	US-09-808-972-2
6	370	100.0	370	4	US-09-823-033-5
7	370	100.0	370	4	US-09-438-046-8
8	370	100.0	370	4	US-09-139-583-37
9	370	100.0	370	4	US-10-039-847A-2
10	370	100.0	370	4	US-09-438-046-6
11	370	100.0	370	4	US-09-564-595D-56
12	370	100.0	370	4	US-09-564-595D-55
13	370	100.0	370	4	US-09-564-595D-57
14	370	100.0	370	4	US-09-438-046-19
15	370	100.0	370	4	US-09-438-046-4
16	370	100.0	370	4	US-09-564-595D-54
17	370	100.0	370	4	US-09-438-046-2
18	370	100.0	370	4	US-09-438-046-18
19	370	100.0	370	4	US-09-540-224-4
20	370	100.0	370	4	US-09-564-595D-53
21	370	100.0	370	4	US-09-808-972-4
22	370	100.0	370	4	US-10-039-847A-4
23	370	100.0	370	4	US-09-540-224-8
24	370	100.0	370	4	US-09-564-595D-40
25	370	100.0	370	4	US-09-808-972-10
26	370	100.0	370	4	US-09-540-224-9
27	370	100.0	370	4	US-09-564-595D-41

28	23	6.2	24	4	US-09-808-972-11	Sequence 11, App1
29	18	4.9	18	4	US-09-540-224-7	Sequence 7, App1
30	18	4.9	18	4	US-09-564-595D-39	Sequence 39, App1
31	18	4.9	18	4	US-09-808-972-9	Sequence 9, App1
32	8	2.2	94	1	US-08-278-089A-31	Sequence 31, App1
33	8	2.2	94	2	US-08-838-957A-30	Sequence 30, App1
34	8	2.2	113	4	US-09-468-647A-99	Sequence 99, App1
35	8	2.2	132	4	US-09-468-647A-29	Sequence 29, App1
36	8	2.2	149	4	US-09-468-647A-124	Sequence 124, App1
37	8	2.2	227	4	US-09-468-647A-114	Sequence 114, App1
38	8	2.2	227	4	US-09-468-647A-116	Sequence 116, App1
39	8	2.2	323	4	US-09-468-647A-1	Sequence 1, App1
40	8	2.2	345	3	US-09-040-220D-2	Sequence 2, App1
41	8	2.2	345	4	US-09-457-066-2	Sequence 43, App1
42	8	2.2	345	4	US-09-457-066-43	Sequence 2, App1
43	8	2.2	345	4	US-09-265-686-2	Sequence 3, App1
44	8	2.2	345	4	US-09-540-224-5	Sequence 5, App1
45	8	2.2	345	4	US-09-564-595D-33	Sequence 33, App1
46	8	2.2	345	4	US-09-564-595D-35	Sequence 35, App1
47	8	2.2	345	4	US-09-706-968-2	Sequence 2, App1
48	8	2.2	345	4	US-09-706-968-43	Sequence 43, App1
49	8	2.2	345	4	US-09-723-749-2	Sequence 2, App1
50	8	2.2	345	4	US-09-823-033-2	Sequence 2, App1
51	8	2.2	345	4	US-09-823-033-4	Sequence 4, App1
52	8	2.2	345	4	US-09-468-647A-2	Sequence 2, App1
53	8	2.2	345	4	US-09-468-647A-101	Sequence 101, App1
54	8	2.2	345	4	US-09-468-647A-103	Sequence 103, App1
55	8	2.2	345	4	US-09-468-647A-110	Sequence 110, App1
56	8	2.2	345	4	US-09-468-647A-130	Sequence 130, App1
57	8	2.2	345	4	US-10-139-583-2	Sequence 2, App1
58	8	2.2	345	4	US-10-139-583-43	Sequence 43, App1
59	8	2.2	354	4	US-09-468-647A-120	Sequence 120, App1
60	8	2.2	355	4	US-09-468-647A-122	Sequence 122, App1
61	8	2.2	374	4	US-09-468-647A-118	Sequence 118, App1
62	8	2.2	1138	1	US-08-323-474-8	Sequence 8, App1
63	8	2.2	1138	2	US-08-469-537A-98	Sequence 98, App1
64	8	2.2	1138	2	US-08-220-240A-5	Sequence 5, App1
65	8	2.2	1150	4	US-09-949-016-7769	Sequence 7769, App1
66	8	1.9	96	4	US-09-248-796A-23698	Sequence 23698, App1
67	7	1.9	111	4	US-09-468-647A-26	Sequence 26, App1
68	7	1.9	113	4	US-09-614-912-186	Sequence 186, App1
69	7	1.9	123	4	US-09-640-211A-728	Sequence 728, App1
70	7	1.9	167	4	US-09-468-647A-111	Sequence 111, App1
71	7	1.9	168	4	US-09-468-647A-27	Sequence 27, App1
72	7	1.9	168	4	US-09-468-647A-126	Sequence 126, App1
73	7	1.9	220	4	US-09-270-767A-45040	Sequence 45040, App1
74	7	1.9	232	4	US-09-834-759-517	Sequence 517, App1
75	7	1.9	240	4	US-09-328-352-4858	Sequence 4858, App1
76	7	1.9	278	4	US-09-834-759-515	Sequence 515, App1
77	7	1.9	282	4	US-09-468-647A-112	Sequence 112, App1
78	7	1.9	301	5	US-08-118-270-72	Sequence 72, App1
79	7	1.9	301	5	PCT-US933-08528-72	Sequence 72, App1
80	7	1.9	325	4	US-09-270-767A-43881	Sequence 43881, App1
81	7	1.9	330	4	US-09-710-279-1086	Sequence 1086, App1
82	7	1.9	339	4	US-09-328-352-6551	Sequence 6551, App1
83	7	1.9	348	3	US-09-134-003C-3294	Sequence 3294, App1
84	7	1.9	352	4	US-09-543-681A-6618	Sequence 6618, App1
85	7	1.9	393	4	US-09-248-796A-18833	Sequence 18833, App1
86	7	1.9	472	4	US-09-489-036A-12395	Sequence 12395, App1
87	7	1.9	541	4	US-08-828-199A-2	Sequence 2, App1
88	7	1.9	647	4	US-09-248-796A-15400	Sequence 15400, App1
89	7	1.9	1016	4	US-09-949-016-11304	Sequence 11304, App1
90	7	1.9	1057	4	US-09-107-533A-4789	Sequence 4789, App1
91	7	1.9	1193	3	US-09-227-725A-4	Sequence 4, App1
92	7	1.9	1211	4	US-09-167-206-14	Sequence 14, App1
93	7	1.9	1286	4	US-09-252-991A-24589	Sequence 24589, App1
94	7	1.9	1344	3	US-09-413-814-46	Sequence 46, App1
95	7	1.9	1871	2	US-08-694-869-1	Sequence 1, App1
96	7	1.9	1871	3	US-09-349-546-1	Sequence 1, App1
97	7	1.9	1871	4	US-09-502-831-1	Sequence 12, App1
98	7	1.9	1901	4	US-09-738-946-12	Sequence 12, App1
99	7	1.9	1956	3	US-08-843-417-2	Sequence 2, App1
100	7	1.9	1956	4	US-09-527-013-2	Sequence 2, App1

ALIGNMENTS

```
RESULT 1
US-09-457-066-37
; Sequence 37, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-37

Query Match      100.0%; Score 370; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLDLYRDETIQYKG 60
DB 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLDLYRDETIQYKG 60
QY 61 NGVQSPRPNSYPNNLLTWRLHSENTRIQLVFNQFGLAEANDICRYDFVEVEDIS 120
DB 61 NGVQSPRPNSYPNNLLTWRLHSENTRIQLVFNQFGLAEANDICRYDFVEVEDIS 120
QY 121 ETSITIRGRWCCHKEVPPRIKSRITNOIKITPKSDDYFVAKPGFKIYSLLEDFOPAASE 180
DB 121 ETSITIRGRWCCHKEVPPRIKSRITNOIKITPKSDDYFVAKPGFKIYSLLEDFOPAASE 180
QY 181 TMSEVTSISISGVNSPSVPTLIDALDKKIAEFTVBDLLKYPNPSMOEDLENNY 240
DB 181 TMSEVTSISISGVNSPSVPTLIDALDKKIAEFTVBDLLKYPNPSMOEDLENNY 240
QY 241 LDTPRYGRSYHDKRSKYVDLRLNDDAKRYSCTPRNYSVINIRELKLAVVFFPRCLLVQ 300
DB 241 LDTPRYGRSYHDKRSKYVDLRLNDDAKRYSCTPRNYSVINIRELKLAVVFFPRCLLVQ 300
QY 301 RCGNGCGGCTVNMWRSCTNSGKTVKHYEVLOFEPGHIKRRGRAKTMAVLDIQLDHERC 360
DB 301 RCGNGCGGCTVNMWRSCTNSGKTVKHYEVLOFEPGHIKRRGRAKTMAVLDIQLDHERC 360
QY 361 DCICSSRPFR 370
DB 361 DCICSSRPFR 370

RESULT 2
US-09-540-224-2
; Sequence 2, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
```

```
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-2

Query Match      100.0%; Score 370; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLDLYRDETIQYKG 60
DB 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLDLYRDETIQYKG 60
QY 61 NGVQSPRPNSYPNNLLTWRLHSENTRIQLVFNQFGLAEANDICRYDFVEVEDIS 120
DB 61 NGVQSPRPNSYPNNLLTWRLHSENTRIQLVFNQFGLAEANDICRYDFVEVEDIS 120
QY 121 ETSITIRGRWCCHKEVPPRIKSRITNOIKITPKSDDYFVAKPGFKIYSLLEDFOPAASE 180
DB 121 ETSITIRGRWCCHKEVPPRIKSRITNOIKITPKSDDYFVAKPGFKIYSLLEDFOPAASE 180
QY 181 TMSEVTSISISGVNSPSVPTLIDALDKKIAEFTVBDLLKYPNPSMOEDLENNY 240
DB 181 TMSEVTSISISGVNSPSVPTLIDALDKKIAEFTVBDLLKYPNPSMOEDLENNY 240
QY 241 LDTPRYGRSYHDKRSKYVDLRLNDDAKRYSCTPRNYSVINIRELKLAVVFFPRCLLVQ 300
DB 241 LDTPRYGRSYHDKRSKYVDLRLNDDAKRYSCTPRNYSVINIRELKLAVVFFPRCLLVQ 300
QY 301 RCGNGCGGCTVNMWRSCTNSGKTVKHYEVLOFEPGHIKRRGRAKTMAVLDIQLDHERC 360
DB 301 RCGNGCGGCTVNMWRSCTNSGKTVKHYEVLOFEPGHIKRRGRAKTMAVLDIQLDHERC 360
QY 361 DCICSSRPFR 370
DB 361 DCICSSRPFR 370

RESULT 3
US-09-564-595D-2
; Sequence 2, Application US/09564595D
; Patent No. 6493668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-595D-2

Query Match      100.0%; Score 370; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 MHRLLFYVTLICANFSCCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETTQVKG 60
| | | | |
Db 1 MHRLLFYVTLICANFSCCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETTQVKG 60
| | | | |
QY 61 NGVQSPRPENSYPRNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDVEVEDIS 120
| | | | |
Db 61 NGVQSPRPENSYPRNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDVEVEDIS 120
| | | | |
QY 121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLEDDQPAASE 180
| | | | |
Db 121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLEDDQPAASE 180
| | | | |
QY 181 TNMESVTSSISGVSYNSPSVTPTLLADALDKKIAEFDVIEDLLKYNPESWQEDLENNY 240
| | | | |
Db 181 TNMESVTSSISGVSYNSPSVTPTLLADALDKKIAEFDVIEDLLKYNPESWQEDLENNY 240
| | | | |
QY 241 LDTPRYRGSRHYDRKSKVDLDRNDADAKRYSCTPRNVSVNIREBLKANVFFPRCLLVQ 300
| | | | |
Db 241 LDTPRYRGSRHYDRKSKVDLDRNDADAKRYSCTPRNVSVNIREBLKANVFFPRCLLVQ 300
| | | | |
QY 301 RCGNGCGCTVNMRSCTCNSGKTVKKYHEVLOEPGHIKRRGAKTMALVDIOLDHHERC 360
| | | | |
Db 301 RCGNGCGCTVNMRSCTCNSGKTVKKYHEVLOEPGHIKRRGAKTMALVDIOLDHHERC 360
| | | | |
QY 361 DCICSSRPPR 370
| | | | |
Db 361 DCICSSRPPR 370
| | | | |

RESULT 4

US-09-706-968-37
; Sequence 37, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gao, Zeren
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706, 968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-706-968-37

Query Match 100.0%; Score 370; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFYVTLICANFSCCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETTQVKG 60
| | | | |
Db 1 MHRLLFYVTLICANFSCCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETTQVKG 60
| | | | |
QY 61 NGVQSPRPENSYPRNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDVEVEDIS 120
| | | | |
Db 61 NGVQSPRPENSYPRNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDVEVEDIS 120
| | | | |
QY 121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLEDDQPAASE 180
| | | | |
Db 121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLEDDQPAASE 180
| | | | |
QY 181 TNMESVTSSISGVSYNSPSVTPTLLADALDKKIAEFDVIEDLLKYNPESWQEDLENNY 240
| | | | |

Db 181 TNMESVTSSISGVSYNSPSVTPTLLADALDKKIAEFDVIEDLLKYNPESWQEDLENNY 240
| | | | |
QY 241 LDTPRYRGSRHYDRKSKVDLDRNDADAKRYSCTPRNVSVNIREBLKANVFFPRCLLVQ 300
| | | | |
Db 241 LDTPRYRGSRHYDRKSKVDLDRNDADAKRYSCTPRNVSVNIREBLKANVFFPRCLLVQ 300
| | | | |
QY 301 RCGNGCGCTVNMRSCTCNSGKTVKKYHEVLOEPGHIKRRGAKTMALVDIOLDHHERC 360
| | | | |
Db 301 RCGNGCGCTVNMRSCTCNSGKTVKKYHEVLOEPGHIKRRGAKTMALVDIOLDHHERC 360
| | | | |
QY 361 DCICSSRPPR 370
| | | | |
Db 361 DCICSSRPPR 370
| | | | |

RESULT 5

US-09-808-972-2
; Sequence 2, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808, 972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235, 295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564, 595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180, 169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164, 463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132, 250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-972-2

Query Match 100.0%; Score 370; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFYVTLICANFSCCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETTQVKG 60
| | | | |
Db 1 MHRLLFYVTLICANFSCCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETTQVKG 60
| | | | |
QY 61 NGVQSPRPENSYPRNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDVEVEDIS 120
| | | | |
Db 61 NGVQSPRPENSYPRNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDVEVEDIS 120
| | | | |
QY 121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLEDDQPAASE 180
| | | | |
Db 121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLEDDQPAASE 180
| | | | |
QY 181 TNMESVTSSISGVSYNSPSVTPTLLADALDKKIAEFDVIEDLLKYNPESWQEDLENNY 240
| | | | |
Db 181 TNMESVTSSISGVSYNSPSVTPTLLADALDKKIAEFDVIEDLLKYNPESWQEDLENNY 240
| | | | |
QY 241 LDTPRYRGSRHYDRKSKVDLDRNDADAKRYSCTPRNVSVNIREBLKANVFFPRCLLVQ 300
| | | | |
Db 241 LDTPRYRGSRHYDRKSKVDLDRNDADAKRYSCTPRNVSVNIREBLKANVFFPRCLLVQ 300
| | | | |
QY 301 RCGNGCGCTVNMRSCTCNSGKTVKKYHEVLOEPGHIKRRGAKTMALVDIOLDHHERC 360
| | | | |

Db 301 RCGNCGGCTVNMRSCTCNSGKTIVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 6
US-09-823-033-5
Sequence 5, Application US/09823033
Patent No. 6663870

GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
FILE REFERENCE: 00-12
CURRENT APPLICATION NUMBER: US/09/823,033
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-033-5

Query Match 100.0%; Score 370; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
Db 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
QY 61 NGYVQSPRPNSYPNRLLTWRLHSGENTRIQLVFDNOFGLEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPNSYPNRLLTWRLHSGENTRIQLVFDNOFGLEAENDICRYDFVEVEDIS 120
QY 121 ETSIIIRGMCQKHEVPRIKSRNTOIKITPKSDYFVAKGPKIYYSLLDFOPAAASE 180
Db 121 ETSIIIRGMCQKHEVPRIKSRNTOIKITPKSDYFVAKGPKIYYSLLDFOPAAASE 180
QY 181 TMSVSTSSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLLKYPNBSWQEDLENNY 240
Db 181 TMSVSTSSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLLKYPNBSWQEDLENNY 240
QY 241 LDTPRYRGRSYHDKRSKYVDLRLNDAKRYSCTPRNSYVNIREELKLANVFFPRCLLVQ 300
Db 241 LDTPRYRGRSYHDKRSKYVDLRLNDAKRYSCTPRNSYVNIREELKLANVFFPRCLLVQ 300
QY 301 RCGNCGGCTVNMRSCTCNSGKTIVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNCGGCTVNMRSCTCNSGKTIVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 7
US-09-438-046-8
Sequence 8, Application US/09438046
Patent No. 6706687

GENERAL INFORMATION:
APPLICANT: ERIKSSON, ULF
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTN, Annica
APPLICANT: UTELA, Macko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik

QY 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
Db 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
QY 61 NGYVQSPRPNSYPNRLLTWRLHSGENTRIQLVFDNOFGLEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPNSYPNRLLTWRLHSGENTRIQLVFDNOFGLEAENDICRYDFVEVEDIS 120
QY 121 ETSIIIRGMCQKHEVPRIKSRNTOIKITPKSDYFVAKGPKIYYSLLDFOPAAASE 180
Db 121 ETSIIIRGMCQKHEVPRIKSRNTOIKITPKSDYFVAKGPKIYYSLLDFOPAAASE 180
QY 181 TMSVSTSSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLLKYPNBSWQEDLENNY 240
Db 181 TMSVSTSSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLLKYPNBSWQEDLENNY 240
QY 241 LDTPRYRGRSYHDKRSKYVDLRLNDAKRYSCTPRNSYVNIREELKLANVFFPRCLLVQ 300
Db 241 LDTPRYRGRSYHDKRSKYVDLRLNDAKRYSCTPRNSYVNIREELKLANVFFPRCLLVQ 300
QY 301 RCGNCGGCTVNMRSCTCNSGKTIVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNCGGCTVNMRSCTCNSGKTIVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 8
US-10-139-583-37
Sequence 37, Application US/10139583
Patent No. 6614965

GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/10/139,583
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/457,066

PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 37
LENGTH: 370
TYPE: PR
ORGANISM: Homo sapiens
US-10-139-583-37

Query Match 100.0%; Score 370; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFYVTLICANFSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRETTIOVKG 60
DB 1 MHRLLFYVTLICANFSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRETTIOVKG 60
QY 61 NGVQSPRFPNSYPRNLLTWRLHSGENTRIQLVFNQFGLBEAENDICRYDEVEVEDIS 120
DB 61 NGVQSPRFPNSYPRNLLTWRLHSGENTRIQLVFNQFGLBEAENDICRYDEVEVEDIS 120
QY 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYYSLEDDPOPAASE 180
DB 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYYSLEDDPOPAASE 180
QY 181 TNMESVTSSISGVSYNSPSVTDPTLADALDKKIAEFDVIEDLLKTFNPESWQEDLENNY 240
DB 181 TNMESVTSSISGVSYNSPSVTDPTLADALDKKIAEFDVIEDLLKTFNPESWQEDLENNY 240
QY 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCTPRNSVNIIRBELKLANVFFPRCLLYQ 300
DB 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCTPRNSVNIIRBELKLANVFFPRCLLYQ 300
QY 301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOPEPHIKRGRAKTALVDIOLDHHERC 360
DB 301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOPEPHIKRGRAKTALVDIOLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 9

US-10-039-847A-2
Sequence 2, Application US/10039847A
Patent No. 6827938
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Topouzis, Stavros
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
FILE REFERENCE: 00-100
CURRENT APPLICATION NUMBER: US/10/039,847A
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/244,479
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 370
TYPE: PR
ORGANISM: Homo sapiens
US-10-039-847A-2

Query Match 100.0%; Score 370; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFYVTLICANFSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRETTIOVKG 60
DB 1 MHRLLFYVTLICANFSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRETTIOVKG 60
QY 61 NGVQSPRFPNSYPRNLLTWRLHSGENTRIQLVFNQFGLBEAENDICRYDEVEVEDIS 120

DB 61 NGVQSPRFPNSYPRNLLTWRLHSGENTRIQLVFNQFGLBEAENDICRYDEVEVEDIS 120
QY 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYYSLEDDPOPAASE 180
DB 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYYSLEDDPOPAASE 180
QY 181 TNMESVTSSISGVSYNSPSVTDPTLADALDKKIAEFDVIEDLLKTFNPESWQEDLENNY 240
DB 181 TNMESVTSSISGVSYNSPSVTDPTLADALDKKIAEFDVIEDLLKTFNPESWQEDLENNY 240
QY 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCTPRNSVNIIRBELKLANVFFPRCLLYQ 300
DB 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCTPRNSVNIIRBELKLANVFFPRCLLYQ 300
QY 301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOPEPHIKRGRAKTALVDIOLDHHERC 360
DB 301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOPEPHIKRGRAKTALVDIOLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 10

US-09-438-046-6
Sequence 6, Application US/09438046
Patent No. 670687
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: IEE, Xuri
APPLICANT: PONTN, Annica
APPLICANT: UTELLA, Marko
APPLICANT: ALTALO, Kari
APPLICANT: OESTMAN, Arne
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
FILE REFERENCE: Ulf Eriksson et al 1064-44833
CURRENT APPLICATION NUMBER: US/09/438,046
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: 60/150,604
EARLIER FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 322
TYPE: PR
ORGANISM: Homo sapiens
US-09-438-046-6

Query Match 87.0%; Score 322; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2,5e-305;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 LYRRETTIOVKGNGVQSPRFPNSYPRNLLTWRLHSGENTRIQLVFNQFGLBEAENDI 108
DB 1 LYRRETTIOVKGNGVQSPRFPNSYPRNLLTWRLHSGENTRIQLVFNQFGLBEAENDI 60
QY 109 CRYDFEVEVEDISTSTIIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYYS 168
DB 61 CRYDFEVEVEDISTSTIIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYYS 120
QY 169 LLEDPOPAASETNMESVTSSISGVSYNSPSVTDPTLADALDKKIAEFDVIEDLLKYFN 228

```
Db 121 LLEDFQPAASETNESTVSSISGVSYNSPSVTDPTLLADALDKKIAEDTVEDLLKTFN 180
Qy 229 PESWEDLENNYLDTPRYGRSYHDKRSKVDLDRINDAKRSCTPRNYSVNIREEKLIA 288
Db 181 PESWEDLENNYLDTPRYGRSYHDKRSKVDLDRINDAKRSCTPRNYSVNIREEKLIA 240
Qy 289 NVFFPRCLLVORCGGCGCTVNNRSCCTNSGKTVKKYHEVLOJEPGHIKRGRAKTMA 348
Db 241 NVFFPRCLLVORCGGCGCTVNNRSCCTNSGKTVKKYHEVLOJEPGHIKRGRAKTMA 300
Qy 349 LVDIQLDHHERCDCICSSRPPR 370
Db 301 LVDIQLDHHERCDCICSSRPPR 322

RESULT 11
US-09-564-595D-56
; Sequence 56, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-56

Query Match 55.9%; Score 207; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-193;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 RDETIQVKGNGYVQSPREFNSYPRNLLTWRLHSGENTRIQLVFNQGLEBAENDICRY 111
Db 1 RDETIQVKGNGYVQSPREFNSYPRNLLTWRLHSGENTRIQLVFNQGLEBAENDICRY 60
Qy 112 DFEVEDISESTIIRGRWCGHKEVPPRKSTNQIKITFKSDDYFVAKPGFKIYSLLE 171
Db 61 DFEVEDISESTIIRGRWCGHKEVPPRKSTNQIKITFKSDDYFVAKPGFKIYSLLE 120
Qy 172 DFQPAASETNESTVSSISGVSYNSPSVTDPTLLADALDKKIAEFDEVEDLLKTFNPES 231
Db 121 DFQPAASETNESTVSSISGVSYNSPSVTDPTLLADALDKKIAEFDEVEDLLKTFNPES 180
Qy 232 WOEDLENNYLDTPRYGRSYHDKRSKV 258
Db 181 WOEDLENNYLDTPRYGRSYHDKRSKV 207

RESULT 12
US-09-564-595D-55
; Sequence 55, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
```

```
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55

Query Match 51.6%; Score 191; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 9.5e-178;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 ETNNESTVSSISGVSYNSPSVTDPTLLADALDKKIAEDTVEDLLKTFNPESWEDLENN 239
Db 126 ETNNESTVSSISGVSYNSPSVTDPTLLADALDKKIAEDTVEDLLKTFNPESWEDLENN 185
Qy 240 YLDPTRYGRSYHDKRSKVDLDRINDAKRSCTPRNYSVNIREEKLIA:NVFFPRCLLV 229
Db 186 YLDPTRYGRSYHDKRSKVDLDRINDAKRSCTPRNYSVNIREEKLIA:NVFFPRCLLV 245
Qy 300 QRCGNGCGCTVNNRSCCTNSGKTVKKYHEVLOJEPGHIKRGRAKTMA:VLDIQLDHH 359
Db 246 QRCGNGCGCTVNNRSCCTNSGKTVKKYHEVLOJEPGHIKRGRAKTMA:VLDIQLDHH 305
Qy 360 CDCICSSRPPR 370
Db 306 CDCICSSRPPR 316
```

```
RESULT 13
US-09-564-595D-57
; Sequence 57, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-57

Query Match 34.6%; Score 128; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 2.1e-116;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


QY	52	RDETTQVKGNGVAVOSRFPNSYPRNLLLMRLHSQENTRIQLVFDNQGFEAEANDICRY	111
Db	1	RDETTQVKGNGVAVOSRFPNSYPRNLLLMRLHSQENTRIQLVFDNQGFEAEANDICRY	60
QY	112	DVEVEDISSETSTIIRGRWCGHKEVPRIKSRNTQIKITPKSDDYFAKDFKLYSLE	171
Db	61	DVEVEDISSETSTIIRGRWCGHKEVPRIKSRNTQIKITPKSDDYFAKDFKLYSLE	120
QY	172	DFQPAAS 179	
Db	121	DFQPAAS 128	

```

RESULT 14
US-09-438-046-19
Sequence 19, Application US/09438046
Patent No. 6706687
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: ALLITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Gert-Henrik
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D,
DNA CODING
FILE REFERENCE: Ulf Eriksson et al 1064-44833
CURRENT APPLICATION NUMBER: US/09/438,046
CURRENT FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: 60/150,604
EARLIER FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS.: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-09-438-046-19

```

[illegible]

RESULT 15
US-09-438-046-4
; Sequence 4, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annika
; APPLICANT: UTRELL, Marko
; APPLICANT: ALLTAHO, Kari

APPLICANT: OESTMAN, Arne
 APPLICANT: HELDIN, Carl-Henrik
 TITLE OF INVENTION: PLASMET-DERIVED GROWTH FACTOR D,
 TITLE OF INVENTION: THEREFOR, AND USES THEREOF
 FILE REFERENCE: Ulf Eriksson et al 1064-44833
 CURRENT FILING DATE: 1999-11-10
 EARLIER APPLICATION NUMBER: 60/157,852
 EARLIER FILING DATE: 1998-11-10
 EARLIER APPLICATION NUMBER: 60/113,997
 EARLIER FILING DATE: 1999-12-28
 EARLIER APPLICATION NUMBER: 60/150,604
 EARLIER FILING DATE: 1999-08-26
 EARLIER APPLICATION NUMBER: 60/157,108
 EARLIER FILING DATE: 1999-10-04
 EARLIER APPLICATION NUMBER: 60/157,756
 EARLIER FILING DATE: 1999-10-05
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 4
 LENGTH: 200
 TYPE: PR1
 ORGANISM: Homo sapiens
 US-03-438-046-4

Query Match	31.6%	Score 117	DB 4	Length 200
Best Local Similarity	100.0%	Prod. No. 7.6e-106		
Matches 117	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	195	YNSPSTVPTLIAADLKDIAEFDVEDILKYFNESWQEDLNNYLDTPRYRGRSYHDR	254	
Db	25	YNSPSTVPTLIAADLKDIAEFDVEDILKYFNESWQEDLNNYLDTPRYRGRSYHDR	84	
Qy	255	KSQVLDRLINDAKARYSCTPRNYSVINIREELKLANVFFPRCLLVQRCGNGCGCTV	311	
Db	85	KSQVLDRLINDAKARYSCTPRNYSVINIREELKLANVFFPRCLLVQRCGNGCGCTV	141	

```

RESULT 16
US-09-564-595D-54
Sequence 54, Application US/09564595D
Patent No. 649566
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIORITY APPLICATION NUMBER: US 09/304,216
PRIORITY FILING DATE: 1999-05-03
PRIORITY APPLICATION NUMBER: US 60/164,463
PRIORITY FILING DATE: 1999-11-10
PRIORITY APPLICATION NUMBER: US 60/180,169
PRIORITY FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 54
LENGTH: 302
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion polypeptide
US-09-564-595D-54

```

Query Match	30.5%	Score 113	DB 4	Length 302			
Best Local Similarity	100.0%	Pred. No. 8	5e-102				
Matches 113	Conservative 0	Mismatches 0	Indels 0	Gaps 0			
QY	258	VDLRLNDADAR	YCTPRNYSVNI	REELKLVNVPFPCCLV	YORGGCGGCTV	VMRSGT	317
Db	190	VDLRLNDADAR	YCTPRNYSVNI	REELKLVNVPFPCCLV	YORGGCGGCTV	VMRSGT	249

Qy 318 CNSGTVKHYHEVLOFEPGHIKRRGRATMALVDIQLDHHERCDCICSSRPPR 370
Db 250 CNSGTVKHYHEVLOFEPGHIKRRGRATMALVDIQLDHHERCDCICSSRPPR 302

RESULT 17
US-09-438-046-2
; Sequence 2, Application US/09438046
; Patent No. 6706687

; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0

US-09-438-046-2
; ORGANISM: Homo sapiens

Query Match 17.8%; Score 66; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 305 NCGCTVWVRSTCTCNSGTVKHYHEVLOFEPGHIKRRGRATMALVDIQLDHHERCDCIC 364
Db 1 NCGCTVWVRSTCTCNSGTVKHYHEVLOFEPGHIKRRGRATMALVDIQLDHHERCDCIC 60

Qy 365 SSRPPR 370
Db 61 SSRPPR 66

RESULT 18
US-09-438-046-18

; Sequence 18, Application US/09438046
; Patent No. 6706687

; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10

; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; TYPE: PRT
; LENGTH: 121
; ORGANISM: Homo sapiens
US-09-438-046-18

Query Match 16.8%; Score 62; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.8e-52;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 SYHDKSKVDDRLNDDAKRYSCTPRNSVNIREEIKLANVFPFRCLLVORCGGCGG 309
Db 1 SYHDKSKVDDRLNDDAKRYSCTPRNSVNIREEIKLANVFPFRCLLVORCGGCGG 60

Qy 310 TV 311
Db 61 TV 62

RESULT 19
US-09-540-224-4
; Sequence 4, Application US/09540224
; Patent No. 6468543

; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZV6GF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-540-224-4

Query Match 7.3%; Score 27; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.8e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 SRTNOIKITFKSDDYFVAKPGFKIYYS 168
Db 142 SRTNOIKITFKSDDYFVAKPGFKIYYS 168

RESULT 20
US-09-564-595D-53

; Sequence 53, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Shepherd, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZV6GF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D

```

; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-564-595D-53
```

```

Query Match          7.3%; Score 27; DB 4; Length 370;
Best Local Similarity 100.0%; Pred.No. 5.8e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      142 SRTNQIKITFKSDDYFVAKPGFKIYYS 168
      ||||||||||||||||||||||||||||
DB      142 SRTNQIKITFKSDDYFVAKPGFKIYYS 168
```

```

RESULT 21
US-09-808-972-4
; Sequence 4, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-808-972-4
```

```

Query Match          7.3%; Score 27; DB 4; Length 370;
Best Local Similarity 100.0%; Pred.No. 5.8e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      142 SRTNQIKITFKSDDYFVAKPGFKIYYS 168
      ||||||||||||||||||||||||||||
DB      142 SRTNQIKITFKSDDYFVAKPGFKIYYS 168
```

```

RESULT 22
US-10-039-847A-4
; Sequence 4, Application US/10039847A
; Patent No. 6827938
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; TITLE OF INVENTION: KIDNEY FUNCTION
```

```

; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039,847A
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-039-847A-4
```

```

Query Match          7.3%; Score 27; DB 4; Length 370;
Best Local Similarity 100.0%; Pred.No. 5.8e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      142 SRTNQIKITFKSDDYFVAKPGFKIYYS 168
      ||||||||||||||||||||||||||||
DB      142 SRTNQIKITFKSDDYFVAKPGFKIYYS 168
```

```

RESULT 23
US-09-540-224-8
; Sequence 8, Application US/09540224
; Patent No. 646543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGR4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-540-224-8
```

```

Query Match          6.5%; Score 24; DB 4; Length 25;
Best Local Similarity 100.0%; Pred.No. 4.9e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      230 ESWQEDLENNYLDTPRYRGRSYHD 253
      ||||||||||||||||||||||||||||
DB      1 ESWQEDLENNYLDTPRYRGRSYHD 24
```

```

RESULT 24
US-09-564-595D-40
; Sequence 40, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGR4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
```

; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-564-595D-40

Query Match 6.5%; Score 24; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 230 ESMQEDLENMYLDTPRYGRSYHD 253
|||
Db 1 ESMQEDLENMYLDTPRYGRSYHD 24

RESULT 25
US-09-808-972-10
; Sequence 10; Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; FILE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-808-972-10

Query Match 6.5%; Score 24; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 230 ESMQEDLENMYLDTPRYGRSYHD 253
|||
Db 1 ESMQEDLENMYLDTPRYGRSYHD 24

Search completed: November 10, 2005, 09:48:22
Job time : 44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:41:13 : Search time 165 Seconds
(without alignments)
938.252 Million cell updates/sec

Title: US-10-606-055-2

Perfect score: 370

Sequence: 1 MHRLLFVYLYLCAFCSCRD.....DQLDHERCDDICSSRPPR 370

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867879 seqs, 418409474 residues

Word size : 5

Total number of hits satisfying chosen parameters: 81591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	100.0	370	9	US-09-823-033-5
2	370	100.0	370	9	US-09-808-972-2
3	370	100.0	370	9	US-09-915-582-56
4	370	100.0	370	11	US-09-876-813-2
5	370	100.0	370	11	US-09-833-245-1482
6	370	100.0	370	13	US-10-086-623-8
7	370	100.0	370	13	US-10-139-583-37
8	370	100.0	370	13	US-10-039-847A-2
9	370	100.0	370	13	US-10-260-539-8
10	370	100.0	370	14	US-10-264-361-5
11	370	100.0	370	14	US-10-258-557-2

12	370	100.0	370	14	US-10-228-559-2	Sequence 2, Appli
13	370	100.0	370	14	US-10-274-638-2	Sequence 2, Appli
14	370	100.0	370	14	US-10-011-364-4	Sequence 56, Appli
15	370	100.0	370	14	US-10-277-802-56	Sequence 2, Appli
16	370	100.0	370	15	US-10-246-091-8	Sequence 8, Appli
17	370	100.0	370	15	US-10-365-095-2	Sequence 2, Appli
18	370	100.0	370	15	US-10-321-962-4	Sequence 2, Appli
19	370	100.0	370	15	US-10-606-055-2	Sequence 2, Appli
20	370	100.0	370	15	US-10-664-432-5	Sequence 2, Appli
21	370	100.0	370	16	US-10-650-284-2	Sequence 5, Appli
22	370	100.0	370	16	US-10-664-432-5	Sequence 5, Appli
23	370	100.0	370	16	US-10-877-623-2	Sequence 2, Appli
24	370	100.0	370	16	US-10-772-927A-9	Sequence 9, Appli
25	370	100.0	370	17	US-10-910-938-2	Sequence 2, Appli
26	370	100.0	370	17	US-10-896-972-56	Sequence 56, Appli
27	370	100.0	370	17	US-10-938-041-2	Sequence 2, Appli
28	370	100.0	370	17	US-10-938-375-5	Sequence 5, Appli
29	370	100.0	370	18	US-10-888-610-5	Sequence 8, Appli
30	370	100.0	370	18	US-10-794-392-8	Sequence 8, Appli
31	370	100.0	370	20	US-11-021-068-37	Sequence 37, Appli
32	370	100.0	370	20	US-11-080-803-2	Sequence 2, Appli
33	370	100.0	370	20	US-11-096-308-2	Sequence 2, Appli
34	347	93.8	347	16	US-10-403-142-46	Sequence 46, Appli
35	323	87.3	364	14	US-10-028-072-186	Sequence 186, App
36	323	87.3	364	14	US-10-140-808-186	Sequence 186, App
37	323	87.3	364	14	US-10-123-904-186	Sequence 186, App
38	323	87.3	364	14	US-10-123-904-186	Sequence 186, App
39	323	87.3	364	14	US-10-140-470-186	Sequence 186, App
40	323	87.3	364	14	US-10-175-746-186	Sequence 186, App
41	323	87.3	364	14	US-10-176-918-186	Sequence 186, App
42	323	87.3	364	14	US-10-176-921-186	Sequence 186, App
43	323	87.3	364	14	US-10-137-865-186	Sequence 186, App
44	323	87.3	364	14	US-10-140-474-186	Sequence 186, App
45	323	87.3	364	14	US-10-142-431-186	Sequence 186, App
46	323	87.3	364	14	US-10-143-114-186	Sequence 186, App
47	323	87.3	364	14	US-10-142-419-186	Sequence 186, App
48	323	87.3	364	14	US-10-123-262-186	Sequence 186, App
49	323	87.3	364	14	US-10-142-433-186	Sequence 186, App
50	323	87.3	364	14	US-10-121-050-186	Sequence 186, App
51	323	87.3	364	14	US-10-141-755-186	Sequence 186, App
52	323	87.3	364	14	US-10-143-032-186	Sequence 186, App
53	323	87.3	364	14	US-10-123-108-186	Sequence 186, App
54	323	87.3	364	14	US-10-123-236-186	Sequence 186, App
55	323	87.3	364	14	US-10-123-261-186	Sequence 186, App
56	323	87.3	364	14	US-10-140-921-186	Sequence 186, App
57	323	87.3	364	14	US-10-140-928-186	Sequence 186, App
58	323	87.3	364	14	US-10-121-045-186	Sequence 186, App
59	323	87.3	364	14	US-10-123-292-186	Sequence 186, App
60	323	87.3	364	14	US-10-123-903-186	Sequence 186, App
61	323	87.3	364	14	US-10-124-819-186	Sequence 186, App
62	323	87.3	364	14	US-10-124-822-186	Sequence 186, App
63	323	87.3	364	14	US-10-140-925-186	Sequence 186, App
64	323	87.3	364	14	US-10-160-498-186	Sequence 186, App
65	323	87.3	364	14	US-10-124-824-186	Sequence 186, App
66	323	87.3	364	14	US-10-127-825A-186	Sequence 186, App
67	323	87.3	364	14	US-10-127-829A-186	Sequence 186, App
68	323	87.3	364	14	US-10-127-835A-186	Sequence 186, App
69	323	87.3	364	14	US-10-127-839A-186	Sequence 186, App
70	323	87.3	364	14	US-10-127-901A-186	Sequence 186, App
71	323	87.3	364	14	US-10-128-693A-186	Sequence 186, App
72	323	87.3	364	14	US-10-131-813A-186	Sequence 186, App
73	323	87.3	364	14	US-10-131-818A-186	Sequence 186, App
74	323	87.3	364	14	US-10-131-823A-186	Sequence 186, App
75	323	87.3	364	14	US-10-131-824A-186	Sequence 186, App
76	323	87.3	364	14	US-10-131-830A-186	Sequence 186, App
77	323	87.3	364	14	US-10-131-837A-186	Sequence 186, App
78	323	87.3	364	14	US-10-137-872A-186	Sequence 186, App
79	323	87.3	364	14	US-10-147-500-186	Sequence 186, App
80	323	87.3	364	14	US-10-147-502-186	Sequence 186, App
81	323	87.3	364	14	US-10-147-515-186	Sequence 186, App
82	323	87.3	364	14	US-10-147-517-186	Sequence 186, App
83	323	87.3	364	14	US-10-147-526-186	Sequence 186, App
84	323	87.3	364	14	US-10-147-527-186	Sequence 186, App

```
85 323 87.3 364 14 US-10-121-041-186 Sequence 186, App
86 323 87.3 364 14 US-10-121-043-186 Sequence 186, App
87 323 87.3 364 14 US-10-121-047-186 Sequence 186, App
88 323 87.3 364 14 US-10-123-215-186 Sequence 186, App
89 323 87.3 364 14 US-10-123-902-186 Sequence 186, App
90 323 87.3 364 14 US-10-123-908-186 Sequence 186, App
91 323 87.3 364 14 US-10-123-909-186 Sequence 186, App
92 323 87.3 364 14 US-10-123-910-186 Sequence 186, App
93 323 87.3 364 14 US-10-124-813-186 Sequence 186, App
94 323 87.3 364 14 US-10-124-817-186 Sequence 186, App
95 323 87.3 364 14 US-10-125-922-186 Sequence 186, App
96 323 87.3 364 14 US-10-125-924-186 Sequence 186, App
97 323 87.3 364 14 US-10-140-860-186 Sequence 186, App
98 323 87.3 364 14 US-10-142-417-186 Sequence 186, App
99 323 87.3 364 14 US-10-147-519-186 Sequence 186, App
100 323 87.3 364 14 US-10-157-782-186 Sequence 186, App
```

ALIGNMENTS

```
RESULT 1
US-09-823-033-5
; Sequence 5, Application US/09823033
; Patent No. US2002004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE.
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-5
```

```
Query Match 100.0%; Score 370; DB 9; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
DB 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
QY 61 NGVQSPFPNSYPNNLLTWRHLSQENTRIQLVFDNQFGLEAENDICRYDFVEVEDIS 120
DB 61 NGVQSPFPNSYPNNLLTWRHLSQENTRIQLVFDNQFGLEAENDICRYDFVEVEDIS 120
QY 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKGPFKIYYSLLDFQPAASE 180
DB 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKGPFKIYYSLLDFQPAASE 180
QY 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKGPFKIYYSLLDFQPAASE 180
DB 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKGPFKIYYSLLDFQPAASE 180
QY 181 TNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFTVEDLLKYFNPESMOEDLEMY 240
DB 181 TNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFTVEDLLKYFNPESMOEDLEMY 240
QY 241 LDTPRYGRSYHDKRSKYVDLRLNDAKRYSCTPRNYSVNI REBELKANVVFPPRCLLVQ 300
DB 241 LDTPRYGRSYHDKRSKYVDLRLNDAKRYSCTPRNYSVNI REBELKANVVFPPRCLLVQ 300
QY 301 RCGNGCGGTVMWSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
DB 301 RCGNGCGGTVMWSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPR 370
DB 361 DCICSSRRPR 370
```

```
RESULT 2
US-09-808-972-2
; Sequence 2, Application US/09808972
; Patent No. US20020064832A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-972-2
```

```
Query Match 100.0%; Score 370; DB 9; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
DB 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
QY 61 NGVQSPFPNSYPNNLLTWRHLSQENTRIQLVFDNQFGLEAENDICRYDFVEVEDIS 120
DB 61 NGVQSPFPNSYPNNLLTWRHLSQENTRIQLVFDNQFGLEAENDICRYDFVEVEDIS 120
QY 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKGPFKIYYSLLDFQPAASE 180
DB 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKGPFKIYYSLLDFQPAASE 180
QY 181 TNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFTVEDLLKYFNPESMOEDLEMY 240
DB 181 TNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFTVEDLLKYFNPESMOEDLEMY 240
QY 241 LDTPRYGRSYHDKRSKYVDLRLNDAKRYSCTPRNYSVNI REBELKANVVFPPRCLLVQ 300
DB 241 LDTPRYGRSYHDKRSKYVDLRLNDAKRYSCTPRNYSVNI REBELKANVVFPPRCLLVQ 300
QY 301 RCGNGCGGTVMWSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
DB 301 RCGNGCGGTVMWSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPR 370
DB 361 DCICSSRRPR 370
```

```
RESULT 3
US-09-915-582-56
; Sequence 56, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: P5723P1
```

```
/ CURRENT APPLICATION NUMBER: US/09/915,582
/ CURRENT FILING DATE: 2001-07-27
/ PRIOR APPLICATION NUMBER: PCT/US01/01431
/ PRIOR FILING DATE: 2001-01-17
/ PRIOR APPLICATION NUMBER: 60/179,065
/ PRIOR FILING DATE: 2000-01-31
/ PRIOR APPLICATION NUMBER: 60/180,628
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: 60/231,968
/ PRIOR FILING DATE: 2000-09-12
/ NUMBER OF SEQ ID NOS: 97
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 56
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-915-582-56

Query Match      100.0%; Score 370; DB 9; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLIFVYTLICANFSCSDTSATPOSASIKALRNANLRDSESNHLDLYRRDETIQVKG 60
DB 1 MRLIFVYTLICANFSCSDTSATPOSASIKALRNANLRDSESNHLDLYRRDETIQVKG 60
QY 61 NGVOSPREPNSYPRNLLTWRLHSGENTRIQLVFNQGLEAENDICRYDFVEVEDIS 120
DB 61 NGVOSPREPNSYPRNLLTWRLHSGENTRIQLVFNQGLEAENDICRYDFVEVEDIS 120
QY 121 ESTTIIRGMCCKEYPPRIKSRTNQIKITPKSDYFVAKPGFKIYYSLLDPQPAASE 180
DB 121 ESTTIIRGMCCKEYPPRIKSRTNQIKITPKSDYFVAKPGFKIYYSLLDPQPAASE 180
QY 181 TWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
DB 181 TWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
QY 241 LPTPRYRGRSYNDRKSKVLDRLNDDAKRYSCTPRYSVNIREELKLANVFFPRCLLVQ 300
DB 241 LPTPRYRGRSYNDRKSKVLDRLNDDAKRYSCTPRYSVNIREELKLANVFFPRCLLVQ 300
QY 301 RCGNCGCGTVMWRSCCTCNSGKTVMKKYHEVLOPEPHIKRRGRAKTMALVDIQLDHHERC 360
DB 301 RCGNCGCGTVMWRSCCTCNSGKTVMKKYHEVLOPEPHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 4
US-09-876-813-2
/ Sequence 2, Application US/09876813
/ Publication No. US20040002140A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Teresa
/ APPLICANT: Hart, Charles E.
/ TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
/ FILE REFERENCE: 99-19
/ CURRENT APPLICATION NUMBER: US/09/876,813
/ CURRENT FILING DATE: 2001-05-06
/ PRIOR APPLICATION NUMBER: US/09/564,595
/ PRIOR FILING DATE: 2000-05-03
/ PRIOR APPLICATION NUMBER: US 09/304,216
/ PRIOR FILING DATE: 1999-05-03
/ PRIOR APPLICATION NUMBER: US 60/164,463
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: US 60/180,169
/ PRIOR FILING DATE: 2000-02-04
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: FastSeq for Windows Version 4.0
```

```
/ SEQ ID NO 2
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-876-813-2

Query Match      100.0%; Score 370; DB 11; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLIFVYTLICANFSCSDTSATPOSASIKALRNANLRDSESNHLDLYRRDETIQVKG 60
DB 1 MRLIFVYTLICANFSCSDTSATPOSASIKALRNANLRDSESNHLDLYRRDETIQVKG 60
QY 61 NGVOSPREPNSYPRNLLTWRLHSGENTRIQLVFNQGLEAENDICRYDFVEVEDIS 120
DB 61 NGVOSPREPNSYPRNLLTWRLHSGENTRIQLVFNQGLEAENDICRYDFVEVEDIS 120
QY 121 ESTTIIRGMCCKEYPPRIKSRTNQIKITPKSDYFVAKPGFKIYYSLLDPQPAASE 180
DB 121 ESTTIIRGMCCKEYPPRIKSRTNQIKITPKSDYFVAKPGFKIYYSLLDPQPAASE 180
QY 181 TWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
DB 181 TWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
QY 241 LPTPRYRGRSYNDRKSKVLDRLNDDAKRYSCTPRYSVNIREELKLANVFFPRCLLVQ 300
DB 241 LPTPRYRGRSYNDRKSKVLDRLNDDAKRYSCTPRYSVNIREELKLANVFFPRCLLVQ 300
QY 301 RCGNCGCGTVMWRSCCTCNSGKTVMKKYHEVLOPEPHIKRRGRAKTMALVDIQLDHHERC 360
DB 301 RCGNCGCGTVMWRSCCTCNSGKTVMKKYHEVLOPEPHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 5
US-09-833-245-1482
/ Sequence 1482, Application US/09833245
/ Publication No. US20040010134A1
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc.
/ TITLE OF INVENTION: Albumin Fusion Proteins
/ FILE REFERENCE: PFS46PCT
/ CURRENT APPLICATION NUMBER: US/09/833,245
/ CURRENT FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/229,358
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: 60/256,931
/ PRIOR FILING DATE: 2000-12-21
/ PRIOR APPLICATION NUMBER: 60/199,384
/ PRIOR FILING DATE: 2000-04-25
/ NUMBER OF SEQ ID NOS: 2267
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1482
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-833-245-1482

Query Match      100.0%; Score 370; DB 11; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLIFVYTLICANFSCSDTSATPOSASIKALRNANLRDSESNHLDLYRRDETIQVKG 60
DB 1 MRLIFVYTLICANFSCSDTSATPOSASIKALRNANLRDSESNHLDLYRRDETIQVKG 60
QY 61 NGVOSPREPNSYPRNLLTWRLHSGENTRIQLVFNQGLEAENDICRYDFVEVEDIS 120
```

```
Db 61 NGYVSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNPGLEAEANDICRYDFVEVEDIS 120
Qy 121 ETSIIIRGMCQKHEVPRIKSRITNOIKITFKSDDYFVAKGPFKLYSLLEDFQPAASE 180
Db 121 ETSIIIRGMCQKHEVPRIKSRITNOIKITFKSDDYFVAKGPFKLYSLLEDFQPAASE 180
Qy 181 TNMESVTSISGVSYNPSVTDPTLIADALDKKIAEFTVEDLLKXFNPEBESWQEDLENNY 240
Db 181 TNMESVTSISGVSYNPSVTDPTLIADALDKKIAEFTVEDLLKXFNPEBESWQEDLENNY 240
Qy 241 LDTPRYGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQ 300
Db 241 LDTPRYGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQ 300
Qy 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEBGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEBGHIKRRGRAKTMALVDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370
```

```
RESULT 6
US-10-086-623-8
; Sequence 8, Application US/10086623
; Publication No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: Li, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: TUTELA, Marko
; APPLICANT: ALTITALO, Kari
; APPLICANT: OESTMAN, Aine
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
; FILE REFERENCE: 1064/448332
; CURRENT APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-623-8
```

```
Query Match 100.0%; Score 370; DB 13; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHRLLFYVTLICANFCSCRDTSATPQASISAKLRNANLRDSENLTLTYRDETIQVKG 60
Db 1 MHRLLFYVTLICANFCSCRDTSATPQASISAKLRNANLRDSENLTLTYRDETIQVKG 60
Qy 61 NGYVSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNPGLEAEANDICRYDFVEVEDIS 120
Db 61 NGYVSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNPGLEAEANDICRYDFVEVEDIS 120
```

```
Qy 121 ETSIIIRGMCQKHEVPRIKSRITNOIKITFKSDDYFVAKGPFKLYSLLEDFQPAASE 180
Db 121 ETSIIIRGMCQKHEVPRIKSRITNOIKITFKSDDYFVAKGPFKLYSLLEDFQPAASE 180
Qy 181 TNMESVTSISGVSYNPSVTDPTLIADALDKKIAEFTVEDLLKXFNPEBESWQEDLENNY 240
Db 181 TNMESVTSISGVSYNPSVTDPTLIADALDKKIAEFTVEDLLKXFNPEBESWQEDLENNY 240
Qy 241 LDTPRYGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQ 300
Db 241 LDTPRYGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQ 300
Qy 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEBGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEBGHIKRRGRAKTMALVDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370
```

```
RESULT 7
US-10-139-583-37
; Sequence 37, Application US/10139583
; Publication No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-583-37
```

```
Query Match 100.0%; Score 370; DB 13; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHRLLFYVTLICANFCSCRDTSATPQASISAKLRNANLRDSENLTLTYRDETIQVKG 60
Db 1 MHRLLFYVTLICANFCSCRDTSATPQASISAKLRNANLRDSENLTLTYRDETIQVKG 60
Qy 61 NGYVSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNPGLEAEANDICRYDFVEVEDIS 120
Db 61 NGYVSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNPGLEAEANDICRYDFVEVEDIS 120
Qy 121 ETSIIIRGMCQKHEVPRIKSRITNOIKITFKSDDYFVAKGPFKLYSLLEDFQPAASE 180
Db 121 ETSIIIRGMCQKHEVPRIKSRITNOIKITFKSDDYFVAKGPFKLYSLLEDFQPAASE 180
Qy 181 TNMESVTSISGVSYNPSVTDPTLIADALDKKIAEFTVEDLLKXFNPEBESWQEDLENNY 240
Db 181 TNMESVTSISGVSYNPSVTDPTLIADALDKKIAEFTVEDLLKXFNPEBESWQEDLENNY 240
Qy 241 LDTPRYGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQ 300
Db 241 LDTPRYGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQ 300
Qy 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEBGHIKRRGRAKTMALVDIQLDHHERC 360
```



```
DB      301 RCGGCGCGTVMNRSTCNSGKTVKKYHEVLQPEPHIKRGRAKTMALVDIOLDHHERC 360
      361 DCICSSRPPR 370
      361 DCICSSRPPR 370
```

RESULT 8

```
US-10-039-847A-2
; Sequence 2, Application US/10039847A
; Publication No. US20020183273A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039,847A
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-847A-2
```

```
Query Match      100.0%; Score 370; DB 13; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 MHRLLFVYLLICANFSCSCDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
DB      1 MHRLLFVYLLICANFSCSCDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
QY      61 NGVQSPRPFPNSYPRNLLLTWRLHSEENTRIQLVFNQGFLEAENDICRYDFVEVEDIS 120
DB      61 NGVQSPRPFPNSYPRNLLLTWRLHSEENTRIQLVFNQGFLEAENDICRYDFVEVEDIS 120
QY      121 ESTIIRGRWCGHKEVPRIKSRINOIKITPKSDYFVAKPGFKIYSLLEDPQPAASE 180
DB      121 ESTIIRGRWCGHKEVPRIKSRINOIKITPKSDYFVAKPGFKIYSLLEDPQPAASE 180
QY      181 TWESVTSSISGVSYNSPSVTPTLLADALDKKIAEFDTVEDLLKYNFESMQEDLENNY 240
DB      181 TWESVTSSISGVSYNSPSVTPTLLADALDKKIAEFDTVEDLLKYNFESMQEDLENNY 240
QY      241 LDTPRYGRGSYHDKRSKVDLDRINDAKRYSCTPRNVSVNIREBELKLANVVFPRCLLVQ 300
DB      241 LDTPRYGRGSYHDKRSKVDLDRINDAKRYSCTPRNVSVNIREBELKLANVVFPRCLLVQ 300
QY      301 RCGGCGCGTVMNRSTCNSGKTVKKYHEVLQPEPHIKRGRAKTMALVDIOLDHHERC 360
DB      301 RCGGCGCGTVMNRSTCNSGKTVKKYHEVLQPEPHIKRGRAKTMALVDIOLDHHERC 360
QY      361 DCICSSRPPR 370
DB      361 DCICSSRPPR 370
```

RESULT 9

```
US-10-260-539-8
; Sequence 8, Application US/10260539
; Publication No. US20030073637A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, ULF
; APPLICANT: MASE, Karin
; APPLICANT: LI, Xuxi
; APPLICANT: FOUTEN, Annica
; APPLICANT: UTELA, Marko
```

```
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES T
; FILE REFERENCE: 1064/4483302
; CURRENT APPLICATION NUMBER: US/10/260,539
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-260-539-8
```

```
Query Match      100.0%; Score 370; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 MHRLLFVYLLICANFSCSCDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
DB      1 MHRLLFVYLLICANFSCSCDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
QY      61 NGVQSPRPFPNSYPRNLLLTWRLHSEENTRIQLVFNQGFLEAENDICRYDFVEVEDIS 120
DB      61 NGVQSPRPFPNSYPRNLLLTWRLHSEENTRIQLVFNQGFLEAENDICRYDFVEVEDIS 120
QY      121 ESTIIRGRWCGHKEVPRIKSRINOIKITPKSDYFVAKPGFKIYSLLEDPQPAASE 180
DB      121 ESTIIRGRWCGHKEVPRIKSRINOIKITPKSDYFVAKPGFKIYSLLEDPQPAASE 180
QY      181 TWESVTSSISGVSYNSPSVTPTLLADALDKKIAEFDTVEDLLKYNFESMQEDLENNY 240
DB      181 TWESVTSSISGVSYNSPSVTPTLLADALDKKIAEFDTVEDLLKYNFESMQEDLENNY 240
QY      241 LDTPRYGRGSYHDKRSKVDLDRINDAKRYSCTPRNVSVNIREBELKLANVVFPRCLLVQ 300
DB      241 LDTPRYGRGSYHDKRSKVDLDRINDAKRYSCTPRNVSVNIREBELKLANVVFPRCLLVQ 300
QY      301 RCGGCGCGTVMNRSTCNSGKTVKKYHEVLQPEPHIKRGRAKTMALVDIOLDHHERC 360
DB      301 RCGGCGCGTVMNRSTCNSGKTVKKYHEVLQPEPHIKRGRAKTMALVDIOLDHHERC 360
QY      361 DCICSSRPPR 370
DB      361 DCICSSRPPR 370
```

RESULT 10

```
US-10-264-361-5
; Sequence 5, Application US/10264361
; Publication No. US20030087870A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/264,361
```

;; CURRENT FILING DATE: 2002-10-03
;; PRIOR APPLICATION NUMBER: US/09/695,121
;; PRIOR FILING DATE: 2000-10-23
;; NUMBER OF SEQ ID NOS: 18
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 5
;; LENGTH: 370
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-264-361-5

Query Match 100.0%; Score 370; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRDSENLTLDRDETIOYKG 60
DB 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRDSENLTLDRDETIOYKG 60
QY 61 NGYVQSPRFNSYPRNLLLTWRHLSQENTRIQLVFNQFGLAEANDICRYDFVEVDIS 120
DB 61 NGYVQSPRFNSYPRNLLLTWRHLSQENTRIQLVFNQFGLAEANDICRYDFVEVDIS 120
QY 121 ETSITIRGRWCGHKEVPPRIKSRITNOIKITFKSDYFVAKGFKIYSLLEDFQPAASE 180
DB 121 ETSITIRGRWCGHKEVPPRIKSRITNOIKITFKSDYFVAKGFKIYSLLEDFQPAASE 180
QY 181 TNWESVTSISGVSNSSVTDPTLIADALDKKIAEFTVEDLKYFNPESMQEDLENNY 240
DB 181 TNWESVTSISGVSNSSVTDPTLIADALDKKIAEFTVEDLKYFNPESMQEDLENNY 240
QY 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCPTPNYSVNI REBLKANVVFPPRCLLVQ 300
DB 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCPTPNYSVNI REBLKANVVFPPRCLLVQ 300
QY 301 RCGNCGCGTNNWRSCTNSGKTVKKYHEVLOFEPFGHIKRRGRAKTALVDIQLDHHERC 360
DB 301 RCGNCGCGTNNWRSCTNSGKTVKKYHEVLOFEPFGHIKRRGRAKTALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 11
US-10-258-557-2
;; Sequence 2, Application US/10258557
;; Publication No. US20030100502A1
;; GENERAL INFORMATION:
;; APPLICANT: Beale, John
;; APPLICANT: Gonzalez-Demhitt, Patricia
;; APPLICANT: Hammond, Lisa
;; APPLICANT: Lu, Jirong
;; APPLICANT: Na, Songqing
;; APPLICANT: Su, Eric
;; APPLICANT: Wlitcher, Derrick
;; TITLE OF INVENTION: TREATING MUSCULOSKELETAL DISORDERS USING LP85 AND ANALOGS THEREOF
;; FILE REFERENCE: X-14392M
;; CURRENT APPLICATION NUMBER: US/10/258,557
;; CURRENT FILING DATE: 2002-10-23
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2
;; LENGTH: 370
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-258-557-2

Query Match 100.0%; Score 370; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRDSENLTLDRDETIOYKG 60

DB 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRDSENLTLDRDETIOYKG 60
QY 61 NGYVQSPRFNSYPRNLLLTWRHLSQENTRIQLVFNQFGLAEANDICRYDFVEVDIS 120
DB 61 NGYVQSPRFNSYPRNLLLTWRHLSQENTRIQLVFNQFGLAEANDICRYDFVEVDIS 120
QY 121 ETSITIRGRWCGHKEVPPRIKSRITNOIKITFKSDYFVAKGFKIYSLLEDFQPAASE 180
DB 121 ETSITIRGRWCGHKEVPPRIKSRITNOIKITFKSDYFVAKGFKIYSLLEDFQPAASE 180
QY 181 TNWESVTSISGVSNSSVTDPTLIADALDKKIAEFTVEDLKYFNPESMQEDLENNY 240
DB 181 TNWESVTSISGVSNSSVTDPTLIADALDKKIAEFTVEDLKYFNPESMQEDLENNY 240
QY 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCPTPNYSVNI REBLKANVVFPPRCLLVQ 300
DB 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCPTPNYSVNI REBLKANVVFPPRCLLVQ 300
QY 301 RCGNCGCGTNNWRSCTNSGKTVKKYHEVLOFEPFGHIKRRGRAKTALVDIQLDHHERC 360
DB 301 RCGNCGCGTNNWRSCTNSGKTVKKYHEVLOFEPFGHIKRRGRAKTALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 12
US-10-226-559-2
;; Sequence 2, Application US/10226559
;; Publication No. US20030105015A1
;; GENERAL INFORMATION:
;; APPLICANT: Gilbertson, Debra G.
;; APPLICANT: Hart, Charles E.
;; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
;; FILE REFERENCE: 00-28
;; CURRENT APPLICATION NUMBER: US/10/226,559
;; CURRENT FILING DATE: 2002-08-23
;; PRIOR APPLICATION NUMBER: US/09/540,224
;; PRIOR FILING DATE: 2000-03-31
;; PRIOR APPLICATION NUMBER: US 60/180,169
;; PRIOR FILING DATE: 2000-02-04
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 370
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-226-559-2

Query Match 100.0%; Score 370; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRDSENLTLDRDETIOYKG 60
DB 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRDSENLTLDRDETIOYKG 60
QY 61 NGYVQSPRFNSYPRNLLLTWRHLSQENTRIQLVFNQFGLAEANDICRYDFVEVDIS 120
DB 61 NGYVQSPRFNSYPRNLLLTWRHLSQENTRIQLVFNQFGLAEANDICRYDFVEVDIS 120
QY 121 ETSITIRGRWCGHKEVPPRIKSRITNOIKITFKSDYFVAKGFKIYSLLEDFQPAASE 180
DB 121 ETSITIRGRWCGHKEVPPRIKSRITNOIKITFKSDYFVAKGFKIYSLLEDFQPAASE 180
QY 181 TNWESVTSISGVSNSSVTDPTLIADALDKKIAEFTVEDLKYFNPESMQEDLENNY 240
DB 181 TNWESVTSISGVSNSSVTDPTLIADALDKKIAEFTVEDLKYFNPESMQEDLENNY 240
QY 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCPTPNYSVNI REBLKANVVFPPRCLLVQ 300

```
Db      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVSVNIRELKLAVVFFPRCLVQ 300
Qy      301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOEPGHIKRGAKTMAVLDIOLDHHERC 360
Db      301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOEPGHIKRGAKTMAVLDIOLDHHERC 360
Qy      361 DCICSSRPPR 370
Db      361 DCICSSRPPR 370

RESULT 13
US-10-274-638-2
; Sequence 2, Application US/10274638
; Publication No. US20030109000A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIZED GROWTH FACTOR AND MATERIALS
; FILE REFERENCE: AND METHODS FOR PRODUCING IT
; FILE REFERENCE: 01-30
; CURRENT APPLICATION NUMBER: US/10/274,638
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 60/346,117
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FaastSeq for windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-274-638-2

Query Match      100.0%; Score 370; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MHRLLFVYTLICANFSCSDRTSATPOSASIKALRNANLRDESNHLLTDLVRRBETIQVKG 60
Db      1 MHRLLFVYTLICANFSCSDRTSATPOSASIKALRNANLRDESNHLLTDLVRRBETIQVKG 60
Qy      61 NGVQSPRPFPNSYPRLLLTWRLHSGQENTRIQLVFNQGLGEAENDICRYDVEVEDIS 120
Db      61 NGVQSPRPFPNSYPRLLLTWRLHSGQENTRIQLVFNQGLGEAENDICRYDVEVEDIS 120
Qy      121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEFPAAASE 180
Db      121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEFPAAASE 180
Qy      181 TWMESTTSSISGVSYNSPSVTDPTLTADALDKIAEFDVIEDLLKTFNPESWQEDLENNY 240
Db      181 TWMESTTSSISGVSYNSPSVTDPTLTADALDKIAEFDVIEDLLKTFNPESWQEDLENNY 240
Qy      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVSVNIRELKLAVVFFPRCLVQ 300
Db      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVSVNIRELKLAVVFFPRCLVQ 300
Qy      301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOEPGHIKRGAKTMAVLDIOLDHHERC 360
Db      301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOEPGHIKRGAKTMAVLDIOLDHHERC 360
Qy      361 DCICSSRPPR 370
Db      361 DCICSSRPPR 370

RESULT 14
US-10-011-364-4
; Sequence 4, Application US/10011364
; Publication No. US20030153495A1
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henry
```

```
APPLICANT: Jeffers, Michael
APPLICANT: Shinkete, Richard
APPLICANT: Prayaga, Richard
APPLICANT: Boldog, Ferenc
APPLICANT: Yang, Weijia
APPLICANT: Burgess, Catherine
APPLICANT: Fernandes, Elma
APPLICANT: Rittman, B.
APPLICANT: Shinkete, Juliette
APPLICANT: Larocheille, William
TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease Using Growth
FILE REFERENCE: Factors
FILE REFERENCE: 15966-557A IBD CIP
CURRENT APPLICATION NUMBER: US/10/011,364
PRIOR APPLICATION NUMBER: 60/246,206
PRIOR FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: 09/992,840
PRIOR FILING DATE: 2001-11-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 370
TYPE: PRF
ORGANISM: Homo sapiens
US-10-011-364-4

Query Match      100.0%; Score 370; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MHRLLFVYTLICANFSCSDRTSATPOSASIKALRNANLRDESNHLLTDLVRRBETIQVKG 60
Db      1 MHRLLFVYTLICANFSCSDRTSATPOSASIKALRNANLRDESNHLLTDLVRRBETIQVKG 60
Qy      61 NGVQSPRPFPNSYPRLLLTWRLHSGQENTRIQLVFNQGLGEAENDICRYDVEVEDIS 120
Db      61 NGVQSPRPFPNSYPRLLLTWRLHSGQENTRIQLVFNQGLGEAENDICRYDVEVEDIS 120
Qy      121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEFPAAASE 180
Db      121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEFPAAASE 180
Qy      181 TWMESTTSSISGVSYNSPSVTDPTLTADALDKIAEFDVIEDLLKTFNPESWQEDLENNY 240
Db      181 TWMESTTSSISGVSYNSPSVTDPTLTADALDKIAEFDVIEDLLKTFNPESWQEDLENNY 240
Qy      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVSVNIRELKLAVVFFPRCLVQ 300
Db      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVSVNIRELKLAVVFFPRCLVQ 300
Qy      301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOEPGHIKRGAKTMAVLDIOLDHHERC 360
Db      301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOEPGHIKRGAKTMAVLDIOLDHHERC 360
Qy      361 DCICSSRPPR 370
Db      361 DCICSSRPPR 370

RESULT 15
US-10-277-802-56
; Sequence 56, Application US/10277802
; Publication No. US20030190707A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/10/277,802
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 09/915,582
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
```

```

; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 56
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-277-802-56

Query Match      100.0%; Score 370; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLRDEDTIQYKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLRDEDTIQYKG 60

Qy 61 NGYVQSPFPNSYPNNLLLTWRLHSQENTRIQLVFDNQGLEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPFPNSYPNNLLLTWRLHSQENTRIQLVFDNQGLEAENDICRYDFVEVEDIS 120

Qy 121 ETSITIRGRWCGHKVEPPRIKSRNQIKITFKSDDYFPAKPGFKIYSLLEDFOPAAASE 180
Db 121 ETSITIRGRWCGHKVEPPRIKSRNQIKITFKSDDYFPAKPGFKIYSLLEDFOPAAASE 180

Qy 181 TNMESVTSSISGVSNPSVTDPTLIADALDKIAEFTVBDLKYPNPESWQEDLENMY 240
Db 181 TNMESVTSSISGVSNPSVTDPTLIADALDKIAEFTVBDLKYPNPESWQEDLENMY 240

Qy 241 LDTPRYRGRSYHDRKSKYVDLRLNDADAKRYSCTPRNSVNIREEKLNAVVFPPRCLLVQ 300
Db 241 LDTPRYRGRSYHDRKSKYVDLRLNDADAKRYSCTPRNSVNIREEKLNAVVFPPRCLLVQ 300

Qy 301 RCGGCGGCTVNMWRSCTNSGKTVKKYHEVLQFEFGHKKRRGRATMALVLDIQLDHHBRC 360
Db 301 RCGGCGGCTVNMWRSCTNSGKTVKKYHEVLQFEFGHKKRRGRATMALVLDIQLDHHBRC 360

Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 16
US-10-246-091-8
; Sequence 8, Application US/10246091
; Publication No. US20030203844A1
; GENERAL INFORMATION:
; APPLICANT: Dellani, Kloumarts
; APPLICANT: Janson, Ann Marie
; APPLICANT: Kuhn, Georg
; APPLICANT: Place, Karlheinz
; APPLICANT: Schnazer, Anne
; APPLICANT: Wachns, Frank-Peter
; APPLICANT: Zhao, Ming
; TITLE OF INVENTION: Treatment of Central Nervous System Disorders
; FILE REFERENCE: 21882-504 (PDGF/VEGF)
; CURRENT APPLICATION NUMBER: US/10/246,091
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,381
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/326,044
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
```

```

; ORGANISM: Homo sapiens
US-10-246-091-8

Query Match      100.0%; Score 370; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLRDEDTIQYKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLRDEDTIQYKG 60

Qy 61 NGYVQSPFPNSYPNNLLLTWRLHSQENTRIQLVFDNQGLEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPFPNSYPNNLLLTWRLHSQENTRIQLVFDNQGLEAENDICRYDFVEVEDIS 120

Qy 121 ETSITIRGRWCGHKVEPPRIKSRNQIKITFKSDDYFPAKPGFKIYSLLEDFOPAAASE 180
Db 121 ETSITIRGRWCGHKVEPPRIKSRNQIKITFKSDDYFPAKPGFKIYSLLEDFOPAAASE 180

Qy 181 TNMESVTSSISGVSNPSVTDPTLIADALDKIAEFTVBDLKYPNPESWQEDLENMY 240
Db 181 TNMESVTSSISGVSNPSVTDPTLIADALDKIAEFTVBDLKYPNPESWQEDLENMY 240

Qy 241 LDTPRYRGRSYHDRKSKYVDLRLNDADAKRYSCTPRNSVNIREEKLNAVVFPPRCLLVQ 300
Db 241 LDTPRYRGRSYHDRKSKYVDLRLNDADAKRYSCTPRNSVNIREEKLNAVVFPPRCLLVQ 300

Qy 301 RCGGCGGCTVNMWRSCTNSGKTVKKYHEVLQFEFGHKKRRGRATMALVLDIQLDHHBRC 360
Db 301 RCGGCGGCTVNMWRSCTNSGKTVKKYHEVLQFEFGHKKRRGRATMALVLDIQLDHHBRC 360

Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 17
US-10-365-095-2
; Sequence 2, Application US/10365095
; Publication No. US20030224488A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Swiderek, Kristine M.
; APPLICANT: Bicks, Carl W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR PREPARING DIMERIC GROWTH FACTORS
; FILE REFERENCE: 01-33
; CURRENT APPLICATION NUMBER: US/10/365,095
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 60/355,882
; PRIOR FILING DATE: 2002-02-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-365-095-2

Query Match      100.0%; Score 370; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLRDEDTIQYKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLRDEDTIQYKG 60

Qy 61 NGYVQSPFPNSYPNNLLLTWRLHSQENTRIQLVFDNQGLEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPFPNSYPNNLLLTWRLHSQENTRIQLVFDNQGLEAENDICRYDFVEVEDIS 120

Qy 121 ETSITIRGRWCGHKVEPPRIKSRNQIKITFKSDDYFPAKPGFKIYSLLEDFOPAAASE 180
Db 121 ETSITIRGRWCGHKVEPPRIKSRNQIKITFKSDDYFPAKPGFKIYSLLEDFOPAAASE 180
```

Db 121 ESTTIRGRWCGHKEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
QY 181 TTMESVTSSISGVSYNSPSTVDTPTLLADALDKKIAEDTVEEDLLKYNFESWQEDLENNY 240
Db 181 TTMESVTSSISGVSYNSPSTVDTPTLLADALDKKIAEDTVEEDLLKYNFESWQEDLENNY 240
QY 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNYSVNIIRBELKLANVFFPRCLLYQ 300
Db 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNYSVNIIRBELKLANVFFPRCLLYQ 300
QY 301 RCGGNCGGCTVNNRSCCTCNSGKTVKKYHEVLOPEPGHIKRGRAKTMALVDIOLDHHERC 360
Db 301 RCGGNCGGCTVNNRSCCTCNSGKTVKKYHEVLOPEPGHIKRGRAKTMALVDIOLDHHERC 360
QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 18

US-10-321-962-4
Sequence 4, Application US/10321962
Publication No. US2004006015A1
GENERAL INFORMATION:
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Fernandes, Elma
APPLICANT: Jeffers, Michael E.
APPLICANT: Larochelelle, William J.
APPLICANT: Lichenstein, Henry S.
APPLICANT: Peterson, Jeffrey
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Rittman, Bech
APPLICANT: Shimkets, Uliette
APPLICANT: Shimkets, Richard A.
APPLICANT: Yang, MeiJia
APPLICANT: Curagen Corporation
TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease
FILE REFERENCE: 15966-557A 1BD CIP2
CURRENT APPLICATION NUMBER: US/10/321,962
CURRENT FILING DATE: 2002-12-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Curaseqlist version 0.1
SEQ ID NO 4
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-10-321-962-4

Query Match 100.0%; Score 370; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFVYTLICANFSCSDRTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIQVKG 60
Db 1 MHRLLFVYTLICANFSCSDRTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIQVKG 60
QY 61 NGVQSPREPNSYPRNLLTWRLHSEENTRIQVLPDNOGFLBEAENDICRYDFVEVEDIS 120
Db 61 NGVQSPREPNSYPRNLLTWRLHSEENTRIQVLPDNOGFLBEAENDICRYDFVEVEDIS 120
QY 121 ESTTIRGRWCGHKEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
Db 121 ESTTIRGRWCGHKEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
QY 181 TTMESVTSSISGVSYNSPSTVDTPTLLADALDKKIAEDTVEEDLLKYNFESWQEDLENNY 240
Db 181 TTMESVTSSISGVSYNSPSTVDTPTLLADALDKKIAEDTVEEDLLKYNFESWQEDLENNY 240
QY 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNYSVNIIRBELKLANVFFPRCLLYQ 300
Db 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNYSVNIIRBELKLANVFFPRCLLYQ 300

QY 301 RCGGNCGGCTVNNRSCCTCNSGKTVKKYHEVLOPEPGHIKRGRAKTMALVDIOLDHHERC 360
Db 301 RCGGNCGGCTVNNRSCCTCNSGKTVKKYHEVLOPEPGHIKRGRAKTMALVDIOLDHHERC 360
QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 19

US-10-606-055-2
Sequence 2, Application US/10606055
Publication No. US20040043027A1
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Topouzis, Stavros
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
FILE REFERENCE: 00-79
CURRENT APPLICATION NUMBER: US/10/606,055
CURRENT FILING DATE: 2003-06-25
PRIOR APPLICATION NUMBER: US/09/808,972
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 60/235,295
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/564,595
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/132,250
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-10-606-055-2

Query Match 100.0%; Score 370; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFVYTLICANFSCSDRTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIQVKG 60
Db 1 MHRLLFVYTLICANFSCSDRTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIQVKG 60
QY 61 NGVQSPREPNSYPRNLLTWRLHSEENTRIQVLPDNOGFLBEAENDICRYDFVEVEDIS 120
Db 61 NGVQSPREPNSYPRNLLTWRLHSEENTRIQVLPDNOGFLBEAENDICRYDFVEVEDIS 120
QY 121 ESTTIRGRWCGHKEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
Db 121 ESTTIRGRWCGHKEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
QY 181 TTMESVTSSISGVSYNSPSTVDTPTLLADALDKKIAEDTVEEDLLKYNFESWQEDLENNY 240
Db 181 TTMESVTSSISGVSYNSPSTVDTPTLLADALDKKIAEDTVEEDLLKYNFESWQEDLENNY 240
QY 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNYSVNIIRBELKLANVFFPRCLLYQ 300
Db 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNYSVNIIRBELKLANVFFPRCLLYQ 300
QY 301 RCGGNCGGCTVNNRSCCTCNSGKTVKKYHEVLOPEPGHIKRGRAKTMALVDIOLDHHERC 360
Db 301 RCGGNCGGCTVNNRSCCTCNSGKTVKKYHEVLOPEPGHIKRGRAKTMALVDIOLDHHERC 360
QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

Db 361 DCICSSRPPR 370

RESULT 20

US-10-664-432-5

Sequence 5, Application US/10664432

Publication No. US20040043031A1

GENERAL INFORMATION:

APPLICANT: Hart, Charles E.

APPLICANT: Gilbertson, Debra G.

TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,

FILE REFERENCE: 00-12

CURRENT APPLICATION NUMBER: US/10/664,432

CURRENT FILING DATE: 2003-09-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 370

TYPE: PRT

ORGANISM: Homo sapiens

US-10-664-432-5

Query Match 100.0%; Score 370; DB 15; Length 370;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDPSNHLTDLRRDETIQVKG 60

Db 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDPSNHLTDLRRDETIQVKG 60

QY 61 NGVOSPRFPNSYPNNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120

Db 61 NGVOSPRFPNSYPNNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120

QY 121 ESTTIRGRCGKHKEVPPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFOPAASE 180

Db 121 ESTTIRGRCGKHKEVPPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFOPAASE 180

QY 181 TMESVTSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLKYFNPESQOEDLENNY 240

Db 181 TMESVTSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLKYFNPESQOEDLENNY 240

QY 241 LDTPRYGRSYHDRSKYVDLRLNDADAKRYSCTPRNSYVNIREEKLAVVFFPRCLLVQ 300

Db 241 LDTPRYGRSYHDRSKYVDLRLNDADAKRYSCTPRNSYVNIREEKLAVVFFPRCLLVQ 300

QY 301 RCGNCGCGCTVWNRSTCNSGKTYKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

Db 301 RCGNCGCGCTVWNRSTCNSGKTYKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY 361 DCICSSRPPR 370

Db 361 DCICSSRPPR 370

RESULT 21

US-10-650-284-2

Sequence 2, Application US/10650284

Publication No. US20040110683A1

GENERAL INFORMATION:

APPLICANT: Hui, Rutai

APPLICANT: Chen, Jingzhou

APPLICANT: Liu, Baohua

APPLICANT: Liu, Yuchang

TITLE OF INVENTION: Cell Proliferation Factor Fwa267

FILE REFERENCE: 043774/268252

CURRENT APPLICATION NUMBER: US/10/650,284

CURRENT FILING DATE: 2003-08-28

PRIOR APPLICATION NUMBER: CN01109260.2

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 370

TYPE: PRT

ORGANISM: Homo sapiens

US-10-650-284-2

Query Match 100.0%; Score 370; DB 16; Length 370;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDPSNHLTDLRRDETIQVKG 60

Db 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDPSNHLTDLRRDETIQVKG 60

QY 61 NGVOSPRFPNSYPNNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120

Db 61 NGVOSPRFPNSYPNNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120

QY 121 ESTTIRGRCGKHKEVPPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFOPAASE 180

Db 121 ESTTIRGRCGKHKEVPPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFOPAASE 180

QY 181 TMESVTSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLKYFNPESQOEDLENNY 240

Db 181 TMESVTSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLKYFNPESQOEDLENNY 240

QY 241 LDTPRYGRSYHDRSKYVDLRLNDADAKRYSCTPRNSYVNIREEKLAVVFFPRCLLVQ 300

Db 241 LDTPRYGRSYHDRSKYVDLRLNDADAKRYSCTPRNSYVNIREEKLAVVFFPRCLLVQ 300

QY 301 RCGNCGCGCTVWNRSTCNSGKTYKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

Db 301 RCGNCGCGCTVWNRSTCNSGKTYKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY 361 DCICSSRPPR 370

Db 361 DCICSSRPPR 370

RESULT 22

US-10-664-432-5

Sequence 5, Application US/10664432

Publication No. US20040228870A9

GENERAL INFORMATION:

APPLICANT: Hart, Charles E.

APPLICANT: Gilbertson, Debra G.

TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,

FILE REFERENCE: 00-12

CURRENT APPLICATION NUMBER: US/10/664,432

CURRENT FILING DATE: 2003-09-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 370

TYPE: PRT

ORGANISM: Homo sapiens

US-10-664-432-5

Query Match 100.0%; Score 370; DB 16; Length 370;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDPSNHLTDLRRDETIQVKG 60

Db 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDPSNHLTDLRRDETIQVKG 60

QY 61 NGVOSPRFPNSYPNNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120

Db 61 NGVOSPRFPNSYPNNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120

QY 121 ESTTIRGRCGKHKEVPPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFOPAASE 180

Db 121 ESTTIRGRCGKHKEVPPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFOPAASE 180

Db 121 ESTTIIRGWCCHKEVPRIKSRNQIKITFKSDYFVAKPGFKIYSLLEDFOPAAASE 180
Qy 181 TWMEVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
Db 181 TWMEVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
Qy 241 LDTPRYGRSYHDRKSKVDLDRNDADAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300
Db 241 LDTPRYGRSYHDRKSKVDLDRNDADAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300
Qy 301 RCGGNCGGCTVWNRSTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGGNCGGCTVWNRSTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 23

US-10-877-623-2
; Sequence 2, Application US/10877623
; Publication No. US20040242850A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/10/877,623
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-877-623-2

Query Match 100.0%; Score 370; DB 16; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLDLYRRDETIOVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLDLYRRDETIOVKG 60
Qy 61 NGVOSPRFPNSYPNNLLTWRLHSQENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
Db 61 NGVOSPRFPNSYPNNLLTWRLHSQENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
Qy 121 ESTTIIRGWCCHKEVPRIKSRNQIKITFKSDYFVAKPGFKIYSLLEDFOPAAASE 180
Db 121 ESTTIIRGWCCHKEVPRIKSRNQIKITFKSDYFVAKPGFKIYSLLEDFOPAAASE 180
Qy 181 TWMEVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
Db 181 TWMEVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
Qy 241 LDTPRYGRSYHDRKSKVDLDRNDADAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300
Db 241 LDTPRYGRSYHDRKSKVDLDRNDADAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300

Qy 301 RCGGNCGGCTVWNRSTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGGNCGGCTVWNRSTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 24

US-10-772-927A-9
; Sequence 9, Application US/10772927A
; Publication No. US20040248796A1
; GENERAL INFORMATION:
; APPLICANT: Aitalo, et al.
; TITLE OF INVENTION: VEGF-B AND PDGF MODULATION OF STEM CELLS
; FILE REFERENCE: 28967/39140B
; CURRENT APPLICATION NUMBER: US/10/772,927A
; PRIOR FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/445,021
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/471,412
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patencin version 3.2
; SEQ ID NO 9
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-772-927A-9

Query Match 100.0%; Score 370; DB 16; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLDLYRRDETIOVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLDLYRRDETIOVKG 60
Qy 61 NGVOSPRFPNSYPNNLLTWRLHSQENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
Db 61 NGVOSPRFPNSYPNNLLTWRLHSQENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
Qy 121 ESTTIIRGWCCHKEVPRIKSRNQIKITFKSDYFVAKPGFKIYSLLEDFOPAAASE 180
Db 121 ESTTIIRGWCCHKEVPRIKSRNQIKITFKSDYFVAKPGFKIYSLLEDFOPAAASE 180
Qy 181 TWMEVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
Db 181 TWMEVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESWQEDLENNY 240
Qy 241 LDTPRYGRSYHDRKSKVDLDRNDADAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300
Db 241 LDTPRYGRSYHDRKSKVDLDRNDADAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300
Qy 301 RCGGNCGGCTVWNRSTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGGNCGGCTVWNRSTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 25

US-10-910-938-2
; Sequence 2, Application US/10910938
; Publication No. US20050031694A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; LIGAMENT AND CARTILAGE USING ZVEGF4

```

; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/10/910,938
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US/10/226,559
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US/09/540,224
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-938-2

```

```

Query Match      100.0%; Score 370; DB 17; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MHRLEFVYTLICANFCSCRDTSATPOSASIKALRYANILRDESNHLLTDLYRDETIQYKG 60
Db 1 MHRLEFVYTLICANFCSCRDTSATPOSASIKALRYANILRDESNHLLTDLYRDETIQYKG 60
QY 61 NGYVQSPRFPNSYPNNLLLTWRHLSQENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRFPNSYPNNLLLTWRHLSQENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120
QY 121 ETSTIIRGRWCGHKEVPRIKRTNQIKITFKSDYFVAKPGFKIYYSLEDFQPAASE 180
Db 121 ETSTIIRGRWCGHKEVPRIKRTNQIKITFKSDYFVAKPGFKIYYSLEDFQPAASE 180
QY 181 TNMESVTSISGVSYNSPSVTPDLIADLDKIAEFTVEDLKYFNPESWQEDLENNY 240
Db 181 TNMESVTSISGVSYNSPSVTPDLIADLDKIAEFTVEDLKYFNPESWQEDLENNY 240
QY 241 LDTPRYRGRSYHDKRSKYDLDRINDAKRYSCTPRNYSVINIREELKLANVVFPRCLLVQ 300
Db 241 LDTPRYRGRSYHDKRSKYDLDRINDAKRYSCTPRNYSVINIREELKLANVVFPRCLLVQ 300
QY 301 RCGGNGCGCTVVMRECTCNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGGNGCGCTVVMRECTCNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

```

Search completed: November 10, 2005, 09:51:13
Job time : 167 secs

Prob. not

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:36:17 ; Search time 40 Seconds

(without alignments)
890.005 Million cell updates/sec

Title: US-10-606-055-2

Perfect score: 370

Sequence: 1 MRLRLFYVYLICANFCSCRD.....DIQLDHERDCICSRPPR 370

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 5

Total number of hits satisfying chosen parameters: 19093

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Listing first 100 summaries

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	269	72.7	370	2	JC7591	spinal cord-derived
2	32	8.6	370	2	JC7592	spinal cord-derived
3	27	7.3	370	2	JC7598	platelet-derived g
4	8	2.2	77	2	S37239	metallochionein-11
5	8	2.2	77	2	S52636	metallochionein-11
6	8	2.2	79	2	TQ2128	metallochionein -
7	8	2.2	80	2	TQ2063	metallochionein-11
8	8	2.2	80	2	TQ3404	metallochionein-11
9	8	2.2	80	2	T12326	metallochionein -
10	8	2.2	80	2	T14387	metallochionein-11
11	8	2.2	80	2	T10087	metallochionein-11
12	8	2.2	81	1	SMUTL	metallochionein-11
13	8	2.2	81	2	S57861	metallochionein-11
14	8	2.2	82	2	TQ7114	metallochionein-11
15	8	2.2	82	2	TQ7076	metallochionein-11
16	8	2.2	82	2	TQ3727	metallochionein-11
17	8	2.2	84	2	TQ3787	metallochionein-11
18	8	2.2	353	2	AB1244	aminopeptidase P h
19	8	2.2	353	2	AF1606	aminopeptidase P h
20	8	2.2	485	1	B37855	glucose-6-phosphat
21	8	2.2	531	2	TQ1415	basic leucine zipper
22	8	2.2	995	2	AB1398	formate dehydrogen
23	8	2.2	995	2	AE1773	formate dehydrogen
24	8	2.2	1138	1	S24066	protein-tyrosine k
25	7	1.9	153	2	G90831	probable endopeptid
26	7	1.9	155	2	B90871	probable endopeptid
27	7	1.9	155	2	C85744	probable endopeptid
28	7	1.9	171	2	T10904	sporamin - sweet p
29	7	1.9	172	1	RKR25	ribulose-bisphosphat

30	7	1.9	174	2	H96688	hypothetical prote
31	7	1.9	175	1	RKR256	ribulose-bisphosph
32	7	1.9	175	1	RKR259	ribulose-bisphosph
33	7	1.9	175	2	TQ2060	hypothetical prote
34	7	1.9	181	2	A71145	hypothetical prote
35	7	1.9	238	2	T48888	probable phosphori
36	7	1.9	245	2	A99163	dipeptide transpor
37	7	1.9	245	2	AH3124	hypothetical prote
38	7	1.9	274	2	A71140	hypothetical prote
39	7	1.9	280	2	H72504	hypothetical prote
40	7	1.9	291	2	T34043	hypothetical prote
41	7	1.9	326	2	A70368	conserved hypothet
42	7	1.9	329	2	B84199	hypothetical prote
43	7	1.9	384	2	S38232	glucose kinase glk
44	7	1.9	330	2	A83828	conserved hypothet
45	7	1.9	335	2	A10878	holocytochrome-c s
46	7	1.9	346	2	A34365	Grpase activating
47	7	1.9	361	2	T39723	ketol-acid reducto
48	7	1.9	363	2	C75387	hypothetical prote
49	7	1.9	405	2	AE0990	probable membrane
50	7	1.9	410	2	AE2621	conserved hypothet
51	7	1.9	410	2	E97403	hypothetical prote
52	7	1.9	419	1	S47692	hypothetical 43.8k
53	7	1.9	419	2	B91169	probable transport
54	7	1.9	419	2	B86015	probable transport
55	7	1.9	497	2	B97729	heat shock protein
56	7	1.9	500	2	B86306	F20D23.26 protein
57	7	1.9	506	1	W2W47	E2 protein - human
58	7	1.9	510	2	B60280	bacillolysin-like
59	7	1.9	510	2	A60280	zinc metalloprotei
60	7	1.9	510	2	AD1100	phycoene dehydroge
61	7	1.9	524	2	A32617	hypothetical prote
62	7	1.9	555	2	TQ2899	hypothetical prote
63	7	1.9	565	2	S56645	chaperonin 60. alpi
64	7	1.9	580	2	I40725	2-isopropylmalate
65	7	1.9	644	2	S63056	probable membrane
66	7	1.9	647	1	S42939	malate dehydrogena
67	7	1.9	679	2	H96613	hypothetical prote
68	7	1.9	749	2	E71275	hypothetical integ
69	7	1.9	772	2	S32859	integrin beta 2 ch
70	7	1.9	1010	2	E70140	hypothetical prote
71	7	1.9	1010	2	AH2553	hypothetical prote
72	7	1.9	1086	2	S74251	phosphorylase kin
73	7	1.9	1093	2	S74250	phosphorylase kin
74	7	1.9	1134	2	TQ4587	hypothetical prote
75	7	1.9	1192	2	G70513	5-methyltetrahydro
76	7	1.9	1276	2	F83086	hypothetical prote
77	7	1.9	1359	2	S49883	nuclear protein ST
78	7	1.9	1792	2	T13939	myosin V - fruit f
79	7	1.9	1871	2	S27938	hypothetical prote
80	7	1.9	1957	2	S68453	sodium channel pro
81	7	1.9	3712	2	S18253	laminin alpha-1 ch
82	7	1.9	34	2	H53480	melanoma antigen-s
83	6	1.6	53	2	S77865	ribosomal protein
84	6	1.6	59	2	H69463	hypothetical prote
85	6	1.6	61	2	D90879	hypothetical prote
86	6	1.6	61	2	F85739	hypothetical prote
87	6	1.6	64	1	APBP2	phage shock protei
88	6	1.6	72	2	A10658	hypothetical prote
89	6	1.6	74	2	T17834	hypothetical prote
90	6	1.6	75	2	E72681	hypothetical prote
91	6	1.6	78	2	T28903	hypothetical prote
92	6	1.6	82	2	C48349	UL28 protein - sai
93	6	1.6	83	2	S17145	6-phosphofructo-2-
94	6	1.6	83	2	E81896	hypothetical prote
95	6	1.6	87	2	E83296	hypothetical prote
96	6	1.6	93	2	D69262	hypothetical prote
97	6	1.6	93	2	AF1331	hypothetical prote
98	6	1.6	96	2	AF1702	hypothetical prote
99	6	1.6	96	2	UQ2011	hypothetical 11k p
100	6	1.6	98	2	T42307	hypothetical prote

ALIGNMENTS

RESULT 1

spinal cord-derived growth factor-B precursor - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C/Accession: JG7591

R/Hamada, T.; Uti-Tel, K.; Imaki, J.; Miyata, Y.

Biochem. Biophys. Res. Commun. 280, 733-737, 2001

A/Title: Molecular cloning of SCGF-B, a novel growth factor homologous to SCDFG/PDGF-C/

A/Reference number: JG7591; MUID:21092670; PMID:11162582

A/Accession: JG7591

A/Molecule type: DNA

A/Residues: 1-370 <HAM>

A/Cross-references: UNIPROT:Q9BWV5; UNIPROT:Q9GZP0; DDBJ:AB033832

C/Genetics:

A/Gene: scdGF-B

F:1-17/Domain: secretory signal sequence #status predicted <SIG>

F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>

F:52-170/Region: CUB domain #status predicted

F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow

F:294-308/Region: conserved motif #status predicted

Query Match

Best Local Similarity 72.7%; Score 269; DB 2; Length 370;

Matches 369; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MRLIFVYTLICANFCSCRDTSATPQASIKALRNANLRDESNHLLTDLVREDETIOYKG 60

1 MRLIFVYTLICANFCSCRDTSATPQASIKALRNANLRDESNHLLTDLVREDETIOYKG 60

61 NGYVSPRPNNYPNNLLTWLHSEENTRIQLVNDNQGLEAENDICRYFVEVDIS 120

61 NGYVSPRPNNYPNNLLTWLHSEENTRIQLVNDNQGLEAENDICRYFVEVDIS 120

121 ETSIIIRGWCCHKVPPRIKRTNQIKTFKSDYFVAKPGFKIYSLIEDFOFAASE 180

121 ETSIIIRGWCCHKVPPRIKRTNQIKTFKSDYFVAKPGFKIYSLIEDFOFAASE 180

161 TNWESVTSSISGVSYNSPSVTDPTLIADLDKRIAEPTVEDLLKYFNPESNQEDLENNY 240

161 TNWESVTSSISGVSYNSPSVTDPTLIADLDKRIAEPTVEDLLKYFNPESNQEDLENNY 240

241 LDTPIYRGRSYDRKSKVDLRLNDARKYSCTPNNYSNRIEELKLANVFPFRCCLVQ 300

241 LDTPIYRGRSYDRKSKVDLRLNDARKYSCTPNNYSNRIEELKLANVFPFRCCLVQ 300

301 RCGNCGCGTAVNRSCCTCNSGKTVKHYHEVLQFEFGHIKRGRAKTMALVDIQLDHERC 360

301 RCGNCGCGTAVNRSCCTCNSGKTVKHYHEVLQFEFGHIKRGRAKTMALVDIQLDHERC 360

361 DCICSSRPR 370

361 DCICSSRPR 370

RESULT 2

spinal cord-derived growth factor-B precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C/Accession: JG7592

R/Hamada, T.; Uti-Tel, K.; Imaki, J.; Miyata, Y.

Biochem. Biophys. Res. Commun. 280, 733-737, 2001

A/Title: Molecular cloning of SCGF-B, a novel growth factor homologous to SCDFG/PDGF-C/

A/Reference number: JG7591; MUID:21092670; PMID:11162582

A/Accession: JG7592

A/Molecule type: mRNA

A/Residues: 1-370 <HAM>

A/Cross-references: UNIPROT:Q9EQT1; DDBJ:AB052170

C/Genetics:

A/Gene: scdGF-B

F:1-17/Domain: secretory signal sequence #status predicted <SIG>

F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>

F:52-170/Region: CUB domain #status predicted

F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow

F:294-308/Region: conserved motif #status predicted

Query Match

Best Local Similarity 8.6%; Score 32; DB 2; Length 370;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

23 ATPOSASIKALRNANLRDESNHLLTDLVRRDE 54

23 ATPOSASIKALRNANLRDESNHLLTDLVRRDE 54

RESULT 3

platelet-derived growth factor-D - mouse

C/Species: Mus musculus (house mouse)

C/Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003

C/Accession: JG7998

R/Zhuo, Y.; Hoyle, G.W.; Zhang, J.; Morris, G.; Laaky, J.A.

Biochem. Biophys. Res. Commun. 308, 126-132, 2003

A/Title: A novel murine PDGF-D splicing variant results in significant differences in pe

A/Reference number: JG7998; PMID:12890490

A/Accession: JG7998

A/Molecule type: mRNA

A/Residues: 1-370 <ZHU>

C/Comment: This protein is a potent mesenchymal cell mitogen and chemotactant involve

C/Genetics:

A/Gene: pdGF-D

A/Introns: 42/2; 110/1; 170/2; 191/2; 258/2; 330/1; 334/2

C/Keywords: Fibrosis; PDGF-D

Query Match

Best Local Similarity 7.3%; Score 27; DB 2; Length 370;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

142 SRTNQIKTFKSDDYFVAKPGFKIYYS 168

142 SRTNQIKTFKSDDYFVAKPGFKIYYS 168

RESULT 4

metallothionein-like protein - white clover

C/Species: Trifolium repens (white clover)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C/Accession: S37239

R/Ellison, N.W.

submitted to the EMBL Data Library, September 1993

A/Description: Sequence analysis of two cDNA clones for metallothionein-like proteins fr

A/Reference number: S37239

A/Accession: S37239

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-77 <ELL>

A/Cross-references: UNIPROT:P43398; EMBL:Z26492; NID:g403326; PIDN:CAA81264.1; PID:g4033

C/Superfamily: metallothionein

Query Match

Best Local Similarity 2.2%; Score 8; DB 2; Length 77;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

302 CGGNCGCG 309

4 CGGNCGCG 11

RESULT 5

S52636

metallothionein - fava bean
C/Species: Vicia faba (fava bean)
C/Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: S52636
R/Polley, R.C.; Singh, K.B.
Plant Mol. Biol. 26, 435-444, 1994
A/Title: Isolation of a Vicia faba metallothionein-like gene: expression in foliar trich
A/Reference number: S52636; PMID:95036014; PMID:7948889
A/Accession: S52636
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-77 <POL>
A/Cross-references: UNIPROT:Q41657; EMBL:X77254; NID:G747905; PIDN:CA54471.1; PID:G7479
C/Superfamily: metallothionein

Query Match 2.2%; Score 8; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGCGCG 309
DB 4 CGGCGCG 11

RESULT 6
JQ2128
metallothionein - soybean
C/Species: Glycine max (soybean)
C/Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C/Accession: JQ2128
R/Kawashima, I.; Inokuchi, Y.; Chino, M.; Kimura, M.; Shimizu, N.
Plant Cell Physiol. 32, 913-916, 1991
A/Title: Isolation of a gene for a metallothionein-like protein from soybean.
A/Reference number: JQ2128
A/Accession: JQ2128
A/Molecule type: mRNA
A/Residues: 1-79 <KAW>
A/Cross-references: UNIPROT:Q7M213
A/Experimental source: seedling, cv. Saxa
C/Comment: This protein participates in detoxification and metabolism of heavy metals th
C/Superfamily: metallothionein
C/Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGCGCG 309
DB 4 CGGCGCG 11

RESULT 7
T02063
metallothionein-like protein - rice
C/Species: Oryza sativa (rice)
C/Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C/Accession: T02063
R/Dee, M.C.; Kim, C.S.; Eun, M.Y.
submitted to the EMBL Data Library, August 1997
A/Description: Characterization of metallothionein-like protein from rice.
A/Reference number: Z14532
A/Accession: T02063
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-80 <LEE>
A/Cross-references: UNIPROT:Q22488; EMBL:AF017365; NID:G2407284; PIDN:AAB70545.1; PID:G2
C/Superfamily: metallothionein

Query Match 2.2%; Score 8; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGCGCG 309
DB 4 CGGCGCG 11

RESULT 8
T03404
metallothionein-like protein - rice
C/Species: Oryza sativa (rice)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C/Accession: T03404
R/Yu, L.H.; Umeda, M.; Liu, J.Y.; Zhao, N.M.; Uchimiya, H.
Gene 206, 29-35, 1998
A/Title: A novel MT gene of rice plants is strongly expressed in the node portion of th
A/Reference number: Z14935; PMID:98121509; PMID:9461411
A/Accession: T03404
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-80 <YUL>
A/Cross-references: UNIPROT:Q04107; EMBL:AB002820; NID:G1944204; PIDN:BA19661.1; PID:G1
C/Superfamily: metallothionein

Query Match 2.2%; Score 8; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGCGCG 309
DB 4 CGGCGCG 11

RESULT 9
T12326
metallothionein - common ice plant
C/Species: Mesembryanthemum crystallinum (common ice plant)
C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C/Accession: T12326
R/Michalowski, C.B.; Bohner, H.J.
submitted to the EMBL Data Library, July 1998
A/Description: A metallothionein homolog from the ice plant Mesembryanthemum crystallinu
A/Reference number: Z17493
A/Accession: T12326
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-80 <MIC>
A/Cross-references: UNIPROT:Q04688; EMBL:AF078912; NID:G3342197; PID:G3342198
C/Superfamily: metallothionein
C/Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGCGCG 309
DB 4 CGGCGCG 11

RESULT 10
T14387
metallothionein-like protein - turnip
C/Species: Brassica rapa (turnip)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14387
R/Kim, H.U.; Kim, J.B.; Yun, C.H.; Kang, S.K.; Chung, T.Y.
Plant Physiol. 108, 863, 1995
A/Title: Nucleotide sequence of cDNA clone encoding a metallothionein-like protein from
A/Reference number: Z18022; PMID:95534519; PMID:7610190
A/Accession: T14387
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-80 <KIM>

A:Cross-references: UNIPROT:Q39269; EMBL:I31940; NID:g967969; PIDN:AAA74958.1; PID:g9679
A:Experimental source: subspecies pekinesis; flower
C:Function:
A:Description: participates in detoxification of heavy metals through metal-thiol binding
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGGC 309
Db 4 CGGNCGGC 11

RESULT 11

metallothionein - castor bean
C:Species: Ricinus communis (castor bean)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10087
R:Vangala, S.; Bailey-Serres, J.
Plant Physiol. 109, 721, 1995
A:Title: Nucleotide sequence of a maize (Zea mays L.) cDNA (Accession No. U29383) coding
A:Reference number: Z16941; MUID:96030260; PMID:7480354
A:Accession: T10087
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-80 <VAN>
A:Cross-references: UNIPROT:P30564; EMBL:I02306; NID:g169712; PID:g169713
A:Experimental source: strain Carmencita; tissue-type cotyledon
C:Genetics:
A:Gene: MTI
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGGC 309
Db 4 CGGNCGGC 11

RESULT 12

metallothionein-like protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: S18069; S57897
R:Takahashi, K.
Submitted to the EMBL Data Library, October 1991
A:Reference number: S18069
A:Accession: S18069
A:Molecule type: mRNA
A:Residues: 1-81 <TAA>
A:Cross-references: UNIPROT:P25860; EMBL:X62818; NID:g16183; PIDN:CAA44630.1; PID:g16184
A:Experimental source: strain Columbia
R:Takahashi, K.
Submitted to the EMBL Data Library, July 1992
A:Reference number: S57897
A:Accession: S57897
A:Molecule type: DNA
A:Residues: 1-81 <TAA>
A:Cross-references: EMBL:D11394; NID:g217856; PIDN:BA01990.1; PID:g217857
C:Genetics:
A:Introns: 22/2
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match 2.2%; Score 8; DB 1; Length 81;

Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGGC 309
Db 4 CGGNCGGC 11

RESULT 13

metallothionein 2a - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S57861
R:Zhou, J.; Goldsbrough, P.B.
Mol. Gen. Genet. 248, 318-328, 1995
A:Title: Structure, organization and expression of the metallothionein gene family in Ar
A:Reference number: S57858; MUID:9604699; PMID:7565594
A:Accession: S57861
A:Molecule type: DNA
A:Residues: 1-81 <ZHO>
A:Cross-references: UNIPROT:P25860
C:Genetics:
A:Gene: MT2a
A:Map position: III
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGGC 309
Db 4 CGGNCGGC 11

RESULT 14

metallothionein-like protein - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T07114
R:Gitlich, A.; Ganai, M.; Stephan, U.W.; Baumelein, H.
Plant Mol. Biol. 37, 701-714, 1998
A:Title: Structure, expression and chromosomal localization of the metallothionein-like
A:Reference number: Z15923; MUID:98349862; PMID:9687073
A:Accession: T07114
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-82 <GIR>
A:Cross-references: UNIPROT:Q40158; EMBL:Z68138; NID:g1103688; PIDN:CAA92243.1; PID:g110
A:Experimental source: cultivar Bonner Best; root
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGGC 309
Db 4 CGGNCGGC 11

RESULT 15

metallothionein type II B - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T07076
R:Whitelaw, C.A.; LeHuquet, J.A.; Thurman, D.A.; Tomsett, A.B.
Submitted to the EMBL Data Library, July 1996

A/Description: The isolation and characterization of type II metallochionein-like genes
A/Reference number: Z15900
A/Accession: T037876
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-82 <WHI>
A/Cross-references: UNIPROT:Q40158; EMBL:L77966; NID:gl449137; PIDN:AB04675.1; PID:gl44
A/Experimental source: strain A11a cralg
C/Genetics:
A/Genes: MTB
A/Intons: 22/2
C/Superfamily: metallochionein
C/Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGGC 309
DB 4 CGGNCGGC 11

RESULT 16
T03727
metallochionein-like protein - rice
C/Species: Oryza sativa (rice)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C/Accession: T03727
R/Chen, W.M.; Hsieh, H.M.; Huang, P.C.
Submitted to the EMBL Data Library, December 1996
A/Description: Signification of two introns in type 2 rice metallochionein-like gene.
A/Reference number: Z15032
A/Accession: T03727
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-82 <CHE>
A/Cross-references: UNIPROT:P94029; EMBL:D89931; PIDN:BA14038.1
A/Experimental source: cv. Tainung 67, root
C/Genetics:
A/Genes: rGMT-2
A/Intons: 22/2; 48/2
C/Superfamily: metallochionein

Query Match 2.2%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGGC 309
DB 4 CGGNCGGC 11

RESULT 17
T03787
metallochionein-like protein - rice
C/Species: Oryza sativa (rice)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T03787
R/lee, M.C.; Park, J.Y.; Kim, Y.H.; Sun, M.Y.
Submitted to the EMBL Data Library, October 1996
A/Description: Molecular cloning and characterization of metallochionein-like protein in
A/Reference number: Z15085
A/Accession: T03787
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-84 <LEB>
A/Cross-references: UNIPROT:P93433; EMBL:X08529; PIDN:CA69845.1
C/Superfamily: metallochionein

Query Match 2.2%; Score 8; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGGC 309
DB 4 CGGNCGGC 11

RESULT 18
AB1244
aminopeptidase P homolog lml1354 [imported] - Listeria monocytogenes (strain EGD-e)
C/Species: Listeria monocytogenes
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AB1244
R/Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/authors: Krefc, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltournam, A.; M
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AB1244
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-353 <GLA>
A/Cross-references: UNIPROT:Q8Y7C9; GB:NC_003210; PIDN:CAC99432.1; PID:gl6410770; GSPDB
A/Experimental source: strain EGD-e
C/Genetics:
A/Genes: lml1354
C/Superfamily: X-Pro aminopeptidase

Query Match 2.2%; Score 8; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 FDTVEDLL 224
DB 76 FDTVEDLL 83

RESULT 19
AF1606
aminopeptidase P homolog lml1391 [imported] - Listeria innocua (strain C11p11262)
C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AF1606
R/Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/authors: Krefc, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltournam, A.; M
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AF1606
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-353 <GLA>
A/Cross-references: UNIPROT:Q92C00; GB:AL592022; PIDN:CAC96622.1; PID:gl6413864; GSPDB:
A/Experimental source: strain C11p11262
C/Genetics:
A/Genes: lml1391
C/Superfamily: X-Pro aminopeptidase

Query Match 2.2%; Score 8; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 FDTVEDLL 224
DB 76 FDTVEDLL 83

RESULT 20

B37855
glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - *Zymomonas mobilis*
C:Species: *Zymomonas mobilis*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: B37855
R:Barnell, W.O.; Yi, K.C.; Conway, T.
J. Bacteriol. 172, 7227-7240, 1990
A:Title: Sequence and genetic organization of a *Zymomonas mobilis* gene cluster that enc
A:Reference number: A37855; MUID:91072278; PMID:2254282
A:Accession: B37855
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-485 <BAR>
A:Cross-references: UNIPROT:P21907; GB:M60615; GB:M37982; NID:g155589; PIDN:AAA27692.1;
C:Superfamily: glucose-6-phosphate dehydrogenase
C:Keywords: oxidoreductase

Query Match 2.2%; Score 8; DB 1; Length 485;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 DRLNDDAK 268
DB 69 DRLNDDAK 76

RESULT 21
T01415
basic leucine zipper protein - maize
C:Species: *Zea mays* (maize)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01415
R:Malsh, J.; Waters, C.A.; Freeling, M.
Genes Dev. 12, 208-218, 1998
A:Title: The maize gene *liguleless2* encodes a basic leucine zipper protein involved in t
A:Reference number: Z14322; MUID:98154557; PMID:9490265
A:Accession: T01415
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-531 <MAL>
A:Cross-references: UNIPROT:Q49067; EMBL:AF036949; NID:g2865393; PIDN:AAC39351.1; PID:g2
C:Genetics:
A:Gene: *liguleless2*
A:Map position: 9

Query Match 2.2%; Score 8; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 DFQPAAS 179
DB 42 DFQPAAS 49

RESULT 22
AB1398
formate dehydrogenase alpha chain homolog lmo2586 [imported] - *Listeria monocytogenes* (s
C:Species: *Listeria monocytogenes*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
C:Accession: AB1398
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshih, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of *Listeria species*.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1398
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-995 <GLA>
A:Cross-references: UNIPROT:Q8Y469; GB:NC_003210; PIDN:CAD00664.1; PID:g16412074; GSPDB:

A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2586
C:Superfamily: NAD-dependent formate dehydrogenase alpha subunit; ferredoxin 2(4Fe-4S) h

Query Match 2.2%; Score 8; DB 2; Length 995;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGCGCG 309
DB 982 CGGCGCG 989

RESULT 23
AE1773
formate dehydrogenase alpha chain homolog lin2731 [imported] - *Listeria innocua* (strain
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
C:Accession: AE1773
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshih, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of *Listeria species*.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1773
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-995 <GLA>
A:Cross-references: UNIPROT:Q92707; GB:AL592022; PIDN:CAC97957.1; PID:g16415267; GSPDB:G
A:Experimental source: strain C1p11262
C:Genetics:
A:Gene: *lin2731*
C:Superfamily: NAD-dependent formate dehydrogenase alpha subunit; ferredoxin 2(4Fe-4S) h

Query Match 2.2%; Score 8; DB 2; Length 995;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGCGCG 309
DB 982 CGGCGCG 989

RESULT 24
S24066
protein-tyrosine kinase (EC 2.7.1.112), receptor type tie precursor - human
C:Species: *Homo sapiens* (man)
C:Date: 19-Feb-1994 #sequence_revision 11-Aug-1995 #text_change 21-Jul-2000
C:Accession: S24066; C38269; T52613
R:Partanen, U.; Armstrong, E.; Maekela, T.P.; Korhonen, J.; Sanberg, M.; Renkonen, R.;
Mol. Cell. Biol. 12, 1698-1707, 1992
A:Title: A novel endothelial cell surface receptor tyrosine kinase with extracellular ep
A:Reference number: S24066; MUID:92195316; PMID:1312667
A:Accession: S24066
A:Molecule type: mRNA
A:Residues: 1-1138 <PAR>
A:Cross-references: EMBL:X60957
R:Partanen, U.; Meekela, T.P.; Alitalo, R.; Lehtvaeslahti, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A:Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A:Reference number: A38268; MUID:91062389; PMID:2247464
A:Accession: C38269
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 981-1034 <PAW>
A:Experimental source: clone JTK14
R:Korhonen, J.; Lahtinen, I.; Halmekyro, M.; Alhonen, L.; Janne, J.; Dumont, D.; Alitalo
Blood 86, 1828-1833, 1995
A:Title: Endothelial-specific gene expression directed by the tie gene promoter in vivo.

A:Reference number: 152613; MUID:95383653; PMID:7655012
 A:Accession: 152613
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>
 A:Cross-references: GB:579347; NID:G1086921; PIDN:AAD14299.1; PID:G4261999
 C:Genetics:
 A:Gene: GDB:TIE; JTK14
 A:Cross-references: GDB:212873; OMIM:600222
 A:Map position: 1p34-1p33
 C:Function:
 A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
 C:Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology; fibronectin tyf
 C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-1138/Product: protein-tyrosine kinase, receptor-type tie #status predicted <MAT>
 F:35-107/Domain: immunoglobulin homology <IM1>
 F:215-255/Domain: EGF homology <EG1>
 F:259-302/Domain: EGF homology <EG2>
 F:306-344/Domain: EGF homology <EG3>
 F:365-428/Domain: immunoglobulin homology <IM2>
 F:449-530/Domain: fibronectin type III repeat homology <FN3A>
 F:542-633/Domain: fibronectin type III repeat homology <FN3B>
 F:642-730/Domain: fibronectin type III repeat homology <FN3C>
 F:761-786/Domain: transmembrane #status predicted <TMM>
 F:837-1114/Domain: protein kinase homology <KIN>
 F:845-853/Region: protein kinase ATP-binding motif
 F:43-105,372-426/Dsulfide bonds: #status predicted
 F:83,161,503,596,709/Binding site: carbohydrate (Aen) (covalent) #status predicted
 F:870,887,979/Active site: Lys, Glu, Asp #status predicted

Query Match 2.2% Score 8; DB 1; Length 1138;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 ETSTIRG 128
 |||||
 Db 700 ETSTIRG 707

RESULT 25

G90831
 Probable endopeptidase [Imported] - Escherichia coli (strain O157:H7, substrain RIMD 05C
 C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C:Accession: G90831
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
 gaeawara, N.; Yaenunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: G90831
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-153 <HAY>
 A:Cross-references: UNIPROT:Q8X704; GB:BA000007; PIDN:BA835046.1; PID:G133361087; GSPDB:C
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: Eca1623
 C:Superfamily: phage PA2 endopeptidase

Query Match 1.9% Score 7; DB 2; Length 153;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 ELKLANY 290
 |||||
 Db 43 ELKLANY 49

Search completed: November 10, 2005, 09:47:35
 Job time : 43 secs

This Page Blank (uspto)